

FIGURE 1

ACTGCACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGA
CCCACCGCGTCCGGGCCGGAGCAGCACGCCGCAGGACCTGGAGCTCCGGCTCGCTTCCCG
CAGCGCTACCCGCCATTCGCCTGCCGCCGGCGCTGGGCTCCTGCCGCTTCTGCTG
CTGCTGCCGCCGCCGGAGGCCAAGAACGACGCCCTGCCACCAGGTGCCGGGGCT
GGTGGACAAGTTAACCAAGGGATGGTGGACACCGCAAAGAACGAAACTTGGCGGGAAACA
CGGCTTGGAGGAAAAGACGCTGTCCAAGTACGAGTCCAGCGAGATTGCCCTGCTGGAGATC
CTGGAGGGCTGTGCAGAGCAGCAGTCGAATGCAATCAGATGCTAGAGGCGCAGGAGGA
GCACCTGGAGGCCTGGCTGCAGCTGAAGAGCGAATATCCTGACTTATTGAGTGGTTT
GTGTGAAGACACTGAAAGTGTGCTGCTCTCCAGGAACCTACGGTCCGACTGTCTGCATGC
CAGGGCGGATCCCAGAGGCCCTGCAGCGGAATGCCACTGCAGCGAGATGGGAGCAGACA
GGCGACGGGTCTGCCGGTGCACATGGGTACCAGGGCCGCTGTGCACTGACTGCATGG
ACGGCTACTTCAGCTCGCTCCGAACGAGACCCACAGCATCTGCACAGCCTGTGACGAGTCC
TGCAAGACGTGCTCGGCCTGACCAACAGAGACTGCAGCGAGTGTGAAGTGGCTGGTGCT
GGACGAGGGCGCTGTGGATGTGGACAGAGTGTGCGGCCGAGCCGCTCCCTGCAGCGCTG
CGCAGTTCTGTAAGAACGCCAACGGCTCCTACACGTGCGAAGAGTGTGACTCCAGCTGTG
GGCTGCACAGGGGAAGGCCAGGAAACTGTAAAGAGTGTATCTGGCTACGCGAGGGAGCA
CGGACAGTGTGCAAGATGTGGACAGTGTCACTAGCAGAAAAAACCTGTGTGAGGAAAAACG
AAAATGCTACAATACTCCAGGGAGCTACGTCTGTGTGTCCTGACGGCTTCGAAGAACG
GAAGATGCCGTGTGCCGCCAGAGGCTGAAGCCACAGAAGGAGAAAGCCGACACAGCT
GCCCTCCCGCAAGACCTGTAATTGCGGACTTACCCCTAAATTATTAGAAGGATGTCC
CGTGGAAAATGTGCCCTGAGGATGCCGTCTCCTGCAGTGGACAGCGGGGGAGAGGCTGC
CTGCTCTCTAACGGTGATTCTCATTGTCCTTAAACAGCTGCATTCTGGTTGTTCTTA
AACAGACTTGTATATTTGATACAGTTCTTGTAATAAAATTGACCATTGTAGGTAATCAGG
AGGAAAAAAAAGGGCGCCGCGACTCTAGAGTCGACCTGCAGAACG
TTGGCCGCCATGGCCAACTTGTTATTGCAGCTTATAATGGTTACAAATAAGCAATAGCA
TCACAAATTTCACAAATAAGCATTTCAGCTAGTTGTGGTTGTCCAAACTC
ATCAATGTATCTTATCATGTCTGGATCGGAATTAAATTGCCGCAGCACCATGCCCTGAAAT
AACCTCTGAAAGAGGAACCTGGTAGGTACCTCTGAGGGCGAAAGAACCCAGCTGTGGAATG
TGTGTCAGTTAGGGTGTGGAAAGTCCCCAGGCTCCAGGCAGGAGAAGTATGCAAGCATGC
ATCTCAATTAGTCAGCAACCCAGTTT

FIGURE 2

><subunit 1 of 1, 353 aa, 0 stop

><MW: 38192, pI: 4.53, NX(S/T): 2

MRLPRRAALGLPLLLLLPAPPEAAKKPTPCHRGRGLVDKFNQGMVDTAKKNFGGGNTAEEKTLSYESSEIRL
LEILEGLCESSDFECNQMLEARQEEHLEAWWLQLKSEYPDLFEWFCVKTLKVCCSPGTYGPDCLACQGGSQRPCSG
NGHCSDGSRQGDGSCRCHMGYQGPLCTDCMDGYFSSLRNEHTSICTACDESCKTCSGLTNRDCGECEVGWLDE
GACVDVDECAAEP PCSAAQFCKNANGSYTCECDSSCVGCTGEGPGNCKECISGYAREHGQCADVDEC SLAEKT
CVRKNENCYNTPGSYVCVCPDGFEETEDACVPPAEEAATEGESPTQLPSREDL

Signal peptide:

amino acids 1-24

N-glycosylation sites.

amino acids 190-194 and 251-255

Glycosaminoglycan attachment sites.

amino acids 149-153 and 155-159

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 26-30

Casein kinase II phosphorylation sites.

amino acids 58-62, 66-70, 86-90, 197-201, 210-214, 255-259, 295-299, 339-343
and 349-353

Tyrosine kinase phosphorylation site.

amino acids 303-310

N-myristoylation sites.

amino acids 44-50, 54-60, 55-61, 81-87, 150-156, 158-164, 164-170, 252-258 and
313-319

Aspartic acid and asparagine hydroxylation site.

amino acids 308-320

EGF-like domain cysteine pattern signature.

amino acids 166-178

Leucine zipper pattern.

amino acids 94-116

FIGURE 3

CAGGTCCAAC TG CACCTCGGTTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTC
GACCTCGACCCACCGCGTCCGCCAGGCCGGAGGCAGCGCCCAGCGTCTAAACGGGAACA
GCCCTGGCTGAGGGAGCTGCAGCGCAGCAGAGTATCTGACGGCGCCAGGTTGCGTAGGTGCG
GCACGAGGAGTTTCCCGCAGCGAGGAGGTCCCTGAGCAGCATGGCCCGAGGAGCGCCTTC
CCTGCCGCCGCGCTCTGGCTCTGGAGCATCCTCTGTGCCTGCTGGCACTGCAGGGGGAGGC
CGGGCCGCCGCAGGAGAGAGCCTGTACCTATGGATCGATGCTCACCAAGGCAAGAGTACTCA
TAGGATTGAAGAAGATATCCTGATTGTTCAGAGGGAAAATGGCACCTTACACATGAT
TTCAGAAAAGCGCAACAGAGAATGCCAGCTATTCTGTCAATATCCATTCCATGAATTTAC
CTGGCAAGCTGCAGGGCAGGCAGAATACTTCTATGAATTCTGTCCTGCGCTCCCTGGATA
AAGGCATCATGGCAGATCCAACCGTCAATGTCCTCTGCTGGAACAGTGCTCACAAAGGCA
TCAGTTGTTCAAGTTGGTTCCCATGTCCTGGAAAACAGGATGGGTGGCAGCATTGAAGT
GGATGTGATTGTTATGAATTCTGAAGGCAACACCATTCTCAAACACCTCAAATGCTATCT
TCTTAAACATGTCAACAAGCTGAGTCCCAGCGGGTGGCGAAATGGAGGCTTTGTAAT
GAAAGACGCATCTGCAGTGTCTGATGGTTCCACGGACCTCACTGTGAGAAAGCCCTTG
TACCCCACGATGTATGAATGGTGGACTTGTGACTCCTGGTTCTGCATCTGCCACCTG
GATTCTATGGAGTGAAC TG GACAAGCAAAGCTCAACCACCTGCTTAATGGAGGGACC
TGTCTACCCCTGGAAAATGTATTGCCCTCCAGGACTAGAGGGAGAGCAGTGTGAAATCAG
CAAATGCCACAACCTGCGAAATGGAGGTAAATGCATTGGTAAAAGCAAATGTAAGTGT
CCAAAGGTTACCAGGGAGACCTCTGTTCAAAGCCTGTCTGCGAGCCTGGCTGTGGTCACAT
GGAACCTGCCATGAACCCAAACAAATGCCAATGTCAGAAAGGTTGGCATGGAAGACACTGCAA
TAAAGGTACGAAGCCAGCCTCATACATGCCCTGAGGCCAGCAGCGCCAGCTCAGGCAGC
ACACGCCCTCACTAAAAAGGCCAGGGAGCGGGGATCCACCTGAATCCAATTACATCTGG
TGAACTCCGACATCTGAAACGTTTAAGTTACACCAAGTTACAGCTTAACTGCTTAACTTTCA
TGTGTTGAATGTTAAATAATGTTCACTTACACTTAAGAATACTGGCTGAAATTATTAGCT
TCATTATAAAATCACTGAGCTGATATTACTCTTCTTTAAGTTCTAAGTACGTCTGTAG
CATGATGGTATAGATTCTTCTGTTCACTGCTTGGGACAGATTATATTATGTCAATTGA
TCAGGTTAAAATTTCACTGAGCTGAGTTGGCAGATATTCTAAACATTACGATTATGGT
GTCTGGGGCAGGGAAACATCAGAAAGGTTAAATTGGCAAAATGCGTAAGTCACAAGAAT
TTGGATGGTGCAGTTAATGTTGAAGTTACAGCATTCTCAGATTATTGTCAGATATTAGAT
GTTTGTACATTAAAATTGCTCTTAATTAAACTCTCAATACAATATATTGACCT
TTACCAATTATTCCAGAGATTCACTGTTAAACAAAAAAATTACACTGTGGTAGTGGCATT
AAACAAATATAATATTCTAAACACAATGAAATAGGAATATAATGTATGAACCTTTGCAT
TGGCTTGAAGCAATATAATATTGTAACAAAACACAGCTCTTACCTAATAAACATTTAT
ACTGTTGTATGTATAAAATAAGGTGCTGTTAGTTTTGGAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAGGGCGGCCGCGACTCTAGAGTCGACCTGCAGAAGCTTGGC
CGCCATGGCCCAACTGTTTATTGCA GCTTATAATG

FIGURE 4

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33094
><subunit 1 of 1, 379 aa, 0 stop
><MW: 41528, pI: 7.97, NX(S/T): 2
MARRSAFPAAALWLWSILLCLLALRAEAGPPQEESLYLWIDAHQARVLIGFEEDILIVSEGK
MAPFTHDFRKAQQRMPAIPVNIHSMNFTWQAAGQAEYFYEFLSLRSLDKGIMADPTVNVPILL
GTVPHKASVVQVGFPCLGKQDGVAAFEVDVIVMNSEGNTILQTPQNAIFFKTCQQAECPGGC
RNGGFCNERRICECPDGFHGPCEKALCTPRCMNGGLCVTPGFCICPPGFYGVNCDKANCST
TCFNGGTCFYPGKCI CPPGLEGEQCEISKCPQPCRNGGKIGKSCKCSKGYQGDLCSPVVC
EPGCGAHGTCHEPNKCQCQEGWHGRHCNKRYEASLIHALRPAGAQLRQHTPSLKKAERRDP
PESNYIW

Signal peptide:

amino acids 1-28

N-glycosylation site.

amino acids 88-92, 245-249

Casein kinase II phosphorylation site.

amino acids 319-323

Tyrosine kinase phosphorylation site.

amino acids 370-378

N-myristoylation sites.

amino acids 184-190, 185-191, 189-195, 315-321

ATP/GTP-binding site motif A (P-loop).

amino acids 285-293

EGF-like domain cysteine pattern signature.

amino acids 198-210, 230-242, 262-274, 294-306, 326-338

FIGURE 5

CGGACGCGTGGCGTCCGGCGGTGCAAGAGCCAGGAGGCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC
CCCCAGCCCACACCTCACCAAGGGCCCAGGAGGCCACCATGTGGCGATGTCCACTGGGCTAC
TGCTGTTGCTGCCGCTGGCTGGCCACTTGGCTCTGGGTGCCAGCAGGGTCGTGGCGCCGG
GAGCTAGCACCAGGGTCTGCACCTGCAGGGCATCCGGACGCCAGGGAGGCCGGTACTGCCAGGA
GCAGGACCTGTGCTGCCGCCGTGCCAGCAGACTGTGCCCTGCCACTCTGGCGCCATCT
GTTACTGTGACCTCTCTGCAACCGCACGGTCTCCGACTGCTGCCCTGACTCTGGGACTTC
TGCCTCGGCGTGCCACCCCTTTCCCCGATCCAAGGATGTATGCATGGAGGTGCTATCTA
TCCAGTCTTGGAACGTACTGGACAACGTAAACCGTTGCACCTGCCAGGAGAACAGGCAGT
GGCATGGTGGATCCAGACATGATCAAAGCCATCAACCAGGGCAACTATGGCTGGCAGGCTGG
GAACCACAGCGCCTCTGGGGCATGACCCCTGGATGAGGGCATTGCTACCGCCTGGCACCA
TCCGCCCATCTCCTCGGTATGAACATGCATGAAATTATAACAGTGTGAACCCAGGGAG
GTGCTTCCCACAGCCTCGAGGCCCTGAGAAGTGGCCAACCTGATTGAGGCCTCTTGA
CCAAGGCAACTGTGAGGCTCTGGGCTTCTCCACAGCAGCTGTGGCATCCGATCGTGTCT
CAATCCATTCTCTGGGACACATGACGCCGTCTGTGCCCCAGAACCTGCTGTCTTGAC
ACCCACCAGCAGCAGGGCTGCCCGGGTGTCTCGATGGTGCTGGTGGTTCTGCGTCG
CCGAGGGGTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCC
CTGCGCCCCCTGTATGATGCACAGCCGAGCCATGGTCGGGGCAAGCGCCAGGCCACTGCC
CACTGCCAACAGCTATGTTAATAACAATGACATCTACCAAGGTCACTCCTGTCTACCGCCT
CGGCTCCAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTCA
TGGAGGTGCACTGAGGACTTCTCCTATAACAGGGAGGCATCTACAGCCACAGCCAGTGAGC
CTTGGGAGGCCAGAGAGATACGCCGCATGGACCCACTCAGTCAAGATCACAGGATGGG
AGAGGAGACGCTGCCAGATGGAAGGACGCTAAATACTGGACTGCCAGGCAACTCCTGGGGCC
CAGCCTGGGGCGAGAGGGCCACTTCCGCATCGTGCAGGGCGTCAATGAGTGCACATCGAG
AGCTTGTGCTGGCGTCTGGGCGCGTGGCATGGAGGACATGGTCATCACTGAGGCTG
CGGGCACACGCCGGTCCGGCTGGATCCAGGCTAACGGCCGGGAAGAGGCCCAATG
GGCGGTGACCCAGCCTGCCGACAGAGGCCGGCGCAGGCCGCCAGGGCGTAAT
CCCGCGCGGGTCTCGCTGACGCAGGCCCGCTGGAGGCCGGCAGGCAGGACTGGCG
GAGCCCCAGACCTCCAGTGGGACGGGCAGGGCTGGCTGGGAAGAGCACAGCTGCAG
ATCCCAGGCCTCTGGCGCCCCACTCAAGACTACCAAGCCAGGACACCTCAAGTCTCCAGC
CCCAATACCCACCCCAATCCGTATTCTTTTTTTTTAGACAGGGTCTGCTCCG
TTGCCCAAGGGTGGAGTGCAGTGGCCCATCAGGGCTCACTGTAACCTCGACTCTGGGTTCA
AGTACCCCTCCACCTCAGCCTCTCAAGTAGCTGGGACTACAGGTGCACCAACACCTGGC
TAATTTTGATTTTGTAAGAGGGGGTCTCACTGTTGCCAGGCTGGTTTCGAAC
CCTGGCTCAAGCGGCCACCTGCCCTCCAAAGTGTGGATTGCAGGATGAGCC
ACTGCACCCAGCCCTGTATTCTTATTCTCAGATATTATTTCTTCACTGTTAAAA
TAAAACCAAAAGTATTGATAAAAAAAAAAA

FIGURE 6

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></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA33223  
><subunit 1 of 1, 164 aa, 1 stop  
><MW: 18359, pI: 7.45, NX(S/T): 1  
MWRCPLGLLLLLPLAGHLALGAQQGRGRRELAPGLHLRGIRDAGGRYCQEQLLCRGRADDC  
ALPYLGAICYCDLFCNRTVSDCCPDFWDFCLGVPPPFPIQGCMHGGRIYPVLGTYWDNCNR  
CTCQENRQWHGGSRHDQSHQPGQLWLAGWEPQRLLGHDPG
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N-glycosylation site.

amino acids 78-82, 161-165

TOMT20245406600

Casein kinase II phosphorylation site.

amino acids 80-84, 117-121, 126-130, 169-173, 205-209, 296-300,
411-415

N-myristoylation site.

amino acids 21-27, 39-45, 44-50, 104-110, 160-164, 224-230,
269-275, 378-384, 442-448

Amidation site.

amino acids 26-30, 318-322

Eukaryotic thiol (cysteine) proteases histidine active site.

amino acids 398-409

FIGURE 7

AGGCTCCTGGCCTTTCCACAGCAAGCTNTGCNATCCGATTGTTGTCTCAAATCCA
ATTCTCTGGGACACATNACGCCTGTCCTTNGCCCCAGAACCTGCTGTCTGTACACCCAC
CAGCAGCAGGGCTGCCCGNTGGCGTCTCGATGGTGCTGGTGGTTCTGCGTCGCCGAGG
GNTGGTGTCTGACCACTGCTACCCCTCTCGGGCGTGAACGAGACGAGGCTGGCCCTGCGC
CCCCCTGTATGATGCACAGCCGAGCATGGTCGGGGCAAGGCCAGGCCACTGCCACTGC
CCCAACAGCTATGTTAATAACAATGACATCTACCAGGTCACTCCTGTCTACCGCCTCGGCTC
CAACGACAAGGAGATCATGAAGGAGCTGATGGAGAATGGCCCTGTCCAAGCCCTATGGAGG
TGCATGAGGACTTCTCCTATAACAAGGGAGGCATCTACAGCCACACGCCAGTGAGCCTTGGG
AGGCCAGAGAGATAACGCCGGCATGGGACCCACTCAG

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FIGURE 8

GCTGCTTGCCTGTTGATGGCAGGCTTGGCCCTGCAGCCAGGCAGTGCCTGCTGTGCTACT
CCTGCAAAGCCCAGGTGAGCAACGAGGATGCCTGCAGGTGGAGAATGCACCCAGCTGGGG
GAGCAGTGCTGGACCCCGCGCATCCGCGCAGTTGGCCTCCTGACCGTCATCAGCAAAGGCTG
CAGCTTGAACTGCGTGGACTCACAGGACTACTACGTGGGCAAGAAGAACATCACGTGCT
GTGACACCGACTTGTGCAACGCCAGCGGGGCCATGCCCTGCAGCCGGCTGCCGCATCCTT
GCGCTGCTCCCTGCACTCGGCTGCTGCTGGGACCCGGCCAGCTATAGGCTCTGGGGGG
CCCCGCTGCAGCCCACACTGGGTGTGGTGCCCCAGGCCTCTGTGCCACTCCTCACAGACCTG
GCCCAGGTGGAGCCTGTCCTGGTCCTGAGGCACATCCTAACGCAAGTCTGACCATGTATGT
CTGCACCCCTGTCCCCCACCCTGACCCTCCATGCCCTCTCCAGGACTCCCACCCGGCAGA
TCAGCTCTAGTGACACAGATCCGCCTGCAGATGGCCCTCAACCCTCTGCTGCTGTTTC
CATGGCCCAGCATTCTCCACCCTTAACCCTGTGCTCAGGCACCCTTCCCCCAGGAAGCCTT
CCCTGCCACCCTATCTATGACTTGAGCCAGGTCTGGTCCGTGGTCCCGGCACCCAGCA
GGGGACAGGCACTCAGGAGGGCCAGTAAGGCTGAGATGAAGTGGACTGAGTAGAACTGG
GGACAAGAGTCGACGTGAGTTCCTGGAGTCTCCAGAGATGGGGCTGGAGGCTGGAGGAA
GGGGCCAGGCTTCACATTTGTGGGCTCCTGAATGGCAGCCTGAGCACGTAGGCCTTT
AATAAACACCTGTTGGATAAGCCAAAAAAA

0 10 20 30 40 50 60 70 80 90

FIGURE 9

MTHRTTTWARRTSRAVTPTCATPAGPMPCSRLPPSLRCSLHSACCSDPASYRLWGAPLQPT
LGVVPQASVPLLTDLAQWEPVLVPEAHPNASLTMYVCTPVPHPDPPMALSRTPTRQISSLDT
DPPADGPSNPLCCCFFGPAFSTLNPVLRHLFPQEAFPAHPIYDLSQVWSVVSPAPSRCQALRRAQ

Signal peptide:

amino acids 1-47

N-glycosylation site.

amino acids 31-35, 74-78, 84-88

Casein kinase II phosphorylation site.

amino acids 22-26, 76-80

N-myristoylation site.

amino acids 56-60

Amidation site.

amino acids 70-74

090015322020204

FIGURE 10

CCACCGCGTCCGAACCTCTCCAGCGATGGGAGCCGCCCTGCTGCCAACCTCACTCTGT
GCTTACAGCTGCTGATTCTCTGCTGTCAAACACTCAGTACGTGAGGGACCAGGGGCCATGACC
GACCAGCTGAGCAGGCGGAGATCCCGAGTACCAACTCTACACCAGGACCAGTGGCAAGCA
CGTCAGGTACCGGGCGTCGCATCTCCGCCACCGCCGAGGACGGCAACAAGTTGCCAAGC
TCATAGTGGAGACGGACACGTTGGCAGCCGGGTTCGCATCAAAGGGCTGAGAGTGAGAAAG
TACATCTGTATGAACAAGAGGGCAAGCTCATCGGAAGCCCAGCGGAAGAGCAAAGACTG
CGTTCACGGAGATCGTCTGGAGAACAACTATAACGCCCTCCAGAACGCCGGCACGAGG
GCTGGTTCATGGCCTTCACCGGCAGGGCGGCCAGGCTCCGCAGGCCAGAAC
CAGCGCGAGGCCACTTCATCAAGCGCCTCTACCAAGGCCAGCTGCCCTCCCCAACACGC
CGAGAACAGCAGTCAGTTGAGTTGTGGCTCCGCCAACCGCCGGACCAAGCGCACAC
GGCGGCCAGCCCTCACGTAGTCTGGAGGCAGGGGCAGCAGGCCCTGGCCGCCTCCC
CACCCCTTCCCTTAATCCAAGGACTGGCTGGGTGGCAGGGAGGCCAGATCCCC
GAGGGAGGACCCCTGAGGGCCCGAAGCATCCGAGCCCCCAGCTGGAAAGGGCAGGCCGGTG
CCCCAGGGCGGCTGGCACAGTGCCCTCCGGACGGTGGCAGGCCCTGGAGAGGAAC
GAGTGTACCCCTGATCTCAGGCCACCAGCCTGCGGCCCTCCAGCCGGCTCCTGAAGCC
CGCTGAAAGGTCAAGCGACTGAAGGCCTGCAGACAACCGTCTGGAGGTGGCTGTCTCAAA
TCTGCTTCTCGGATCTCCCTCAGTCTGCCCTCAGGAAACCTCCTGGCTAGACTGTA
GGAAGGGACTTTGTTGTTGTTGTTCAAGAAAAAAGAAAGGGAGAGAGAGGAAAATAG
AGGGTTGTCCACTCCTCACATTCCACGACCCAGGCCTGCACCCACCCCCACTCCCAGCCC
CGGAATAAAACCATTTCTGC

FIGURE 11

MGAARLLPNLTLCLQLLILCCQTQYVRDQGAMTDQLSRRQIREYQLYSRTSGKHVQVTGRRI
SATAEDGNKFAKLIVETDTFGSRVRIKGAESEKYICMNKRGKLIGKPSGKSKDGVFTEIVLE
NNYTAFQNARHEGWFMAFTRQGRPRQASRSRQNQREAHFIKRLYQGQLPFPNHAEKQKQFEEF
VGSAPTRRTKRTRRPQPLT

Signal peptide:

amino acids 1-22

N-glycosylation site.

amino acids 9-13, 126-130

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 60-64

Casein kinase II phosphorylation site.

amino acids 65-69

Tyrosine kinase phosphorylation site.

amino acids 39-48, 89-97

N-myristoylation site.

amino acids 69-75, 188-194

Amidation site.

amino acids 58-62

HBGF/FGF family signature.

amino acids 103-128

FIGURE 12

ACTTGCCATCACCTGTTGCCAGTGTGGAAAATTCTCCCTGTTGAATTTGCACATGGAG
GACAGCAGCAAAGAGGGCAACACAGGCTGATAAGACCAGAGACAGCAGGGAGATTATTTAC
CATACGCCCTCAGGACGTTCCCTCTAGCTGGAGTTCTGGACTTCAACAGAACCCCACATCCAGT
CATTGGATTTGCTGTTATTTTTCTTTTCTTCCACACATTGTATTTAT
TTCCGTACTTCAGAAATGGGCCTACAGACCACAAAGTGGCCAGCCATGGGCTTTTCCT
GAAGTCTTGGCTTATCATTCCCTGGGGCTCTACTCACAGGTGTCACAGGTTCTGACCTCAGTGC
CTAGTGTGTGCCGCTCGACAGGAACCTTGCTACTGTAATGAGCGAAGCTGACCTCAGTG
CCTCTGGGATCCGGAGGGCGTAACCGTACTCTACCTCCACAACAACAAATTAATAATGC
TGGATTCCTGCAGAACTGCACAATGTACAGTCGGTGACACGGCTACCTGTATGGCAACC
AACTGGACGAATTCCCCATGAACCTTCCAAGAATGTCAGAGTTCTCCATTGCAAGGAAAAC
AATATTGAGACCAATTTCACGGCTGCTTGCCCCAGCTCTGAAAGCTTGAAGAGCTGCACCT
GGATGACAACCTCCATATCCACAGTGGGGTGGAAAGACGGGGCTTCCGGGAGGCTATTAGCC
TCAAATTGTTGTTTGTCTAAGAATCACCTGAGCAGTGTGCCTGTTGGCTTCCGTGGAC
TTGCAAGAGCTGAGAGTGGATGAAATCGAATTGCTGTCATATCCGACATGGCCTCCAGAA
TCTCACGAGCTGGAGCGTCTATTGTTGACGGGAACTCCCTGACCAACAAGGGTATGCCG
AGGGCACCTCAGCCATCTCACCAAGCTCAAGGAATTTCATGTAATTGCTGTCC
CACCCCTCCTCCCGATCTCCAGGTACGCATCTGATCAGGCTCTATTGCAAGGACAACAGAT
AAACACATTCTTGTACAGCCTCTCAAATCTGCTAAGCTGGAACGGCTGGATATATCCA
ACAACCAACTCGGGATGCTGACTCAAGGGTTTGATAATCTCCAACCTGAAGCAGCTC
ACTGCTCGGAATAACCCCTGGTTTGACTGCAGTATTAAATGGTCACAGAATGGCTCAA
ATATATCCCTCATCTCTCAACGTGCGGGTTCATGTCGAAGGTCTGAACAAGTCCGG
GGATGGCCGTAGGGAATTAAATGAAATCTTGTCCCTGTCACCACGACCCCCGGCCTG
CCTCTCTCACCCAGCCCCAAGTACAGCTCTCCGACCAACTCAGCCTCCACCCCTCTAT
TCCAAACCTAGCAGAAGCTACACGCCTCCAACCTCCTACCACTCGAAACTTCCCACGATT
CTGACTGGGATGGCAGAGAAAGAGTGACCCCCACCTATTCTGAACGGATCCAGCTCTATC
CATTGTTGAAATGATACTTCCATTCAAGTCAGCTGGCTCTCTTCAACCGTATGGCATA
CAAACTCACATGGGTGAAATGGGCCACAGTTAGTAGGGGGCATGTTCAGGAGCGCATAG
TCAGCGGTGAGAAGCAACACCTGAGCCTGGTTAACCTAGAGCCCCGATCCACCTATCGGATT
TGTTAGTGCCACTGGATGCTTTAACCTACCGCGCGGTAGAAGACACCATTGTTAGAGGC
CACCAACCATGCCCTCTATCTGAACAAACGGCAGCAACACAGCGTCCAGCCATGAGCAGACGA
CGTCCCACAGCATGGCTCCCCCTTCTGCTGGGGCTTGTGATGGGGGGCGCGGTGATATT
GTGCTGGTGGTCTTGTCTAGCGTCTTGTGGCATATGCACAAAAAGGGCGCTACACCTC
CCAGAAAGTGGAAATACAACCGGGCCGGAAAGATGATTATTGCGAGGCAGGCACCAAGA
AGGACAACCTCCATCCTGGAGATGACAGAAACCAAGTTAGATCGTCTCTAAATAACGAT
CAACTCTAAAGGAGATTCAGACTGCAGCCATTACACCCAAATGGGGCATTAAATT
CACAGACTGCCATATCCCCAACACATGCGATACTGCAACAGCAGCGTCCAGACCTGGAGC
ACTGCCATACTGACCAGCCAGAGGCCAGCGTTATCAAGGCAGACAATTAGACTCTTGAGAA
CACACTCGTGTGCACATAAAGACACGCAGATTACATTGATAATGTTACACAGATGCAT
TTGTCATTTGAATACTCTGTAATTATACGGTGTACTATATAATGGGATTTAAAAAGTG
CTATCTTCTATTCAAGTTAACAGTTGTAACCTTGCTTTAAATCTT

FIGURE 13

MGLQTTKWPShGAFFLKSLLIISLGLYSQVSLLACPSVCRCDRNFVYCNERSLTSVPLGIP
EGVTVLYLHNNQINNAGFPaelHNVQSVHTVLYGNQLDEFPMNLPKNVRVLHLQENNIQTI
SRAALAQLLKLEELHDDNSISTVGVEDGAFREAISLKLFLSKNHLSVPVGLPVDLQELR
VDENRIAVISDMAFQNLTSLERLIVDGNLLTNKGIAEGTFSHLTKEFSIVRNSLSHPPPD
LPGTHLIRLYLQDNQINHIPLTAFSNLRKLERLDISNNQLRMLTQGVFDNLSNLKQLTARNN
PWFCDCSIKWVTEWLKYIPSSLNVRGFMCGPEQVRGMARRELNMNLLSCPTTPGLPLFTP
APSTASPTTQPPTLSIPNPSRSYTPPTTSLPTIPDWDRERVTPISERIQLSIHFVND
TSIQVSWLSQLFTVMAYKLTWVKGHSIVGGIVQERIVSGEKQHLSLVNLEPRSTYRICLVPL
DAFNRYRAVEDTICSEATTHASYLNNGSNTASSHEQTTSHSMGSPFLLAGLIGGAVIFVLVVL
LSVFCWHMHKKGRYTSQWKYNRGRRKDDYCEAGTKKDNSILEMTETSQIVSLNNNDQLLKG
DFRLQPIYTPNGGINYTDCHIPNNMRYCNSSVPDLEHCHT

Signal peptide:

amino acids 1-42

Transmembrane domain:

amino acids 542-561

N-glycosylation site.

amino acids 202-206, 298-302, 433-437, 521-525, 635-639, 649-653

Casein kinase II phosphorylation site.

amino acids 204-208, 407-411, 527-531, 593-597, 598-602, 651-655

Tyrosine kinase phosphorylation site.

amino acids 319-328

N-myristoylation site.

amino acids 2-8, 60-66, 149-155, 213-219, 220-226, 294-300,
522-528, 545-551, 633-639

Amidation site.

amino acids 581-585

Leucine zipper pattern.

amino acids 164-186

Phospholipase A2 aspartic acid active site.

amino acids 39-50

FIGURE 14

ACTTGGAGCAAGCGGCGGGCGGAGACAGAGGCAGAGGCAGAAGCTGGGCTCCGTCTGCCCTCCACGAGCG
ATCCCCGAGGAGAGCCGCGCCCTCGCGAGGCAGAGGCCAGAGGAAGACCCGGGTGGCTGCCCTCGCC
TCGCTTCCCAGGCAGCGCTGAGCCTTGCCTCCCTGCCAGGGCAGGGAGCGGTACGTGGGAGGTCCATCT
CTAGGGCAGACACGCTGGACCCACCCGAGACGGCCCTCTGGAGAGTCTGTGAGAACAAAGCAGACC
TGGTTTCATCATTGACAGCTCGCAGTGTCAACACCCATGACTATGCAAAGGTCAAGGAGTTCATCGTGGACA
TCTTGCATTCTTGACATTGGTCTGTGACCCGAGTGGGCTGCTCCAATGGCAGCACTGTCAAGAAATG
AGTTCTCCCTCAAGACCTCAAGAGGAAGTCCGAGGTGGAGCGTGTCAAGAGGATGCCGATCTGTCCACCG
GCACCATGACTGGCTGGCATCCAGTATGCCCTGAACATCGCATTCTCAGAAGCAGAGGGGCCCCCTGA
GGGAGAATGTGCCACGGGTCAATAATGATCGACAGATGGGAGACCTCAGGACTCCGTGCCAGGGTGGCTGCTA
AGGCACGGGACACGGGCATCCTAATCTTGCCATTGGTGTGGCCAGGTAGACTTCAACACCTGAAGTCCATTG
GGAGTGAGCCCCATGAGGACCATGTCCTCCTGTGGCCAATTTCAGCCAGATTGAGACGCTGACCTCCGTGTTCC
AGAAGAAGTTGTGCACGGCCACATGTGCAGCACCTGGAGCATACTGTGCCACTCTGCATCACATCCCTG
GCTCATACGTCTGCAGGTGCAAACAAGGCTACATTCTCAACTCGGATCAGACGACTTGCGAATCCAGGATCTGT
GTGCCATGGAGGACCAACTGTGAGCAGCTGTGTGAATGTGCCGGCTCTCGTGTCCAGTGCTACAGTG
GCTACGCCCTGGCTGAGGATGGGAAGAGGTGTGGCTGTGACTACTGTGCCCTAGAAAACCACGGATGTGAAC
ATGAGTGTGAAATGCTGATGGCTCTACCTTGCCAGTGCCTGAAGGATTGCTTTAACCCAGATGAAAAAA
CGTGACAAGGATCAACTACTGTGCACTGAACAAACCGGGCTGTGAGCATGAGTGCCTAACATGGAGGAGAGCT
ACTACTGCCGCTGCCACCGTGGCTACACTCTGGACCCAAATGGAAAACCTGCAGCCAGTGGACCCTGTGCAC
AGCAGGACCATGGCTGTGAGCAGCTGTGTGAACACGGAGGATTCTCGTGTCCAGTGCTCAGAAGGCTTCC
TCATCAACGAGGACCTCAAGACCTGTCCTCCGGTGGATTACTGCCTGCTGAGTGACCATGGTGTGAATACTCCT
GTGTCACATGGACAGATCCTTGCTGTCACTGTCTGAGGGACACGTGCTCCGCAGCGATGGGAAGACGTGTG
AAAATTGGACTCTTGCTCTGGGGACACGGTGTGAACATTGCTGTGAAGCAGTGAAGATTGTTGTTGTTG
GCCAGTGTGAAAGGTTATATACTCCGTGAAGATGGAAAACCTGCAGAAGGAAAGATGCTGCCAAGCTATAG
ACCATGGCTGTGAACACATTGTTGACTACAGTGCAGACTCATACACGTGCGAGTGCTTGAGGGATTCCGGCTCG
CTGAGGATGGGAAACGCTGCCGAAGGAAGGATGTCTGCACCATGGCTGCCAACACATTGTTGTTGTTG
ATAATGGGAAATTCTACATCTGCAAATGCTCAGAGGGATTGTTCTAGCTGAGGACGGAAAGACGGTGCAGAAAT
GCACTGAAGGCCAATTGACCTGGCTTGATGGATCCAAGAGTCTGGAGGAAGAGAATTGAGGTGCTCCAGT
TGAAGCAGTTGTCACTGAAATTAGATTCTGACAAATTCCCCAAAGCCGCTGAGTGGGCTGCTCCAGT
ATTCCACACAGGTCCACACAGAGTCACTCTGAGAAACTCAGCCAAAGACATGAAAAAGCCGTGGCCC
ACATGAAATACATGGGAAAGGGCTTATGACTGGCTGCCCTGAAACACATGTTGAGAGAAGTTTACCCAAG
GAGAAGGGGCCAGGCCCTTCCACAAGGGTGCCAGAGCAGCCATTGTTCAACGGACGGACGGCTCAGGATG
ACGTCCTGGAGTGGCCAGTAAAGCCAAGGCCATGGTATCACTATGTATGCTGTTGGGTTAGGAAAGCCATG
AGGAGGAACATACAAGAGATTGCTCTGAGCCACAAACAAGCATCTTCTATGCCGAAGACTCAGCACAATGG
ATGAGATAAGTAAAAACTCAAGAAAGGCATCTGTGAAGCTCTAGAAGACTCCGATGGAAGACAGGACTCTCCAG
CAGGGAACTGCCAAAAACGGTCCAACAGCAACAGAAATCTGAGCCAGTCACCATAAATATCCAAGACCTACTTT
CCTGTTCTAAATTGCACTGAGTGCACACAGATATCTGTTGAGAAGACAATCTTACGGTCTACACAAAGCTTT
CCCATTCAACAAACCTTCAGGAAGCCCTTGAGAAGAAAACACGATCAATGCAAATGTGAAAACCTTATAATGT
TCCAGAACCTTGCACAGAACAGTAAGAAAATTACACAGCGCTTAGAAGAAATGACACAGAGAATGGAAGCCC
TGGAAAATGCCAGATAACAGATGAAGATTAGAAATCGCGACACATTGAGTCATTGATCAGGATTACAAT
GAACCGAGTGCAGAGGCCAAAGCTCAGGCTATTGTTAAATCAATAATGTTGAGTAAAACAATCAGTACTGA
GAAACCTGGTTGCCACAGAACAAAGACAAGAAGTACACTAACTGTATAAATTATCTAGGAAAAAAATCCT
TCAGAATTCTAAAGATGAATTACAGGTGAGAATGAATAAGCTATGCAAGGTATTGTAATATACTGTGGACAC
AACTGCTCTGCCTCATCCTGCCTAGTGTGCAATCTCATTGACTATACGATAAAGTTGCACAGTCTTACTT
CTGAGAACACTGCCATAGGAAATGTTGACTGGACTTACCTGATATATGTATATGGATGTATG
CATAAAATCATAGGACATATGTACTTGGAACAAGTTGGATTAAATACATATTAAACCACTTCAG

FIGURE 15

MEKMLAGCFLILGQIVLLPAEARERSGRSISRGRHARTHPTALLESSCENKRADLVFII
DSSRSVNTHDYAKVKEFIVDILQFLDIGPDVTRVGLLQYGSTVKNEFLKTFKRKSEVERAV
KMRHLSTGTMGLAIQYALNIAFSEAEGARPLRENVPRVIMIVTDGRPQDSVAEVAAKARD
TGILIFAIVGQVDFNTLKSIGSEPHEDHVFLVANFSQIETLTSVFQKKCTAHMCSTLEHN
CAHFCINIPGSYVCRCKQGYILNSDQTTCRIDLCAMEDHNCEQLCVNPVPGSFVCQCYSGYA
LAEDGKRCVAVDYCASENHGCEHECVNADGSYLCQCHEGFALNPDEKTCTRINYCALNKG
EHECVNMEESYYCRCHRGYTLDPNGKTCRVDHCAQQDHGCEQLCLNTEDSFVCQCSEGFLI
NEDLKTCSRVDYCLLSDHGCEYSCVNMDRSFACQCPEGHVLRSQDGKTCAKLDSCALGDHGCE
HSCVSSEDSFVCQCPEGYILREDGKTCRRKDVCQAIDHGCEHICVNSDDSYTCECLEGFRILA
EDGKRCRRKDVKCKSTHGCEHICVNNNGNSYICKCSEGFLAEDGRRCKCTEGPIDLVFVID
GSKSLGEENFEVVKQFVTGIIDS LTISPKAARVGLLQYSTQVHTEFTLRNFNSAKDMKKAVA
HMKYMGKGSMTGLALKHMFERSFTQGEGARPLSTRVPRAAIVFTDGRAQDDVSEWASKAKAN
GITMYAVGVGKAIEEEELQEIASEPTNKHLFYAEDFSTMDEISEKLKKGICEALESDSDGRQDS
PAGELPKTVQQPTESEPVTINIQDLLSCSNFAVQHRYLFEEDNLLRSTQKLSHSTKPSGSPL
EEKHDQCKCENLIMFQNLANEEVRKLTQRLEEMTQRMEALENRLRYR

Signal peptide:

amino acids 1-23

N-glycosylation site.

amino acids 221-225

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 115-119, 606-610, 892-896

Casein kinase II phosphorylation site.

amino acids 49-53, 118-122, 149-153, 176-180, 223-227, 243-247,
401-405, 442-446, 501-505, 624-628, 673-677, 706-710, 780-784,
781-785, 819-823, 866-870

N-myristoylation site.

amino acids 133-139, 258-264, 299-305, 340-346, 453-459, 494-500,
639-645, 690-696, 752-758, 792-798

Amidation site.

amino acids 314-318, 560-564, 601-605

Aspartic acid and asparagine hydroxylation site.

amino acids 253-265, 294-306, 335-347, 376-388, 417-423, 458-464,
540-546, 581-587

FIGURE 16

GGAGCCGCCCTGGGTGTCAGCGGCTCGCTCCCGCGCACGCTCCGGCGTCGCAGCCTCG
GCACCTGCAGGTCCGTGCGTCCCGCGCTGGCGCCCTGACTCCGTCCCGCCAGGGAGGGC
CATGATTTCCCTCCCCGGCCCTGGTGACCAACTTGCTGCGGTTTTGTTCTGGGCTGA
GTGCCCTCGCGCCCCCTCGGGGCCAGCTGCAACTGCACCTGCCGCCAACCGGTTGCAG
GCGGTGGAGGGAGGGAAAGTGGTGCTCCAGCGTGGTACACCTGCACGGGGAGGTGTCTC
ATCCCAGCCATGGGAGGTGCCCTTGATGTGGTTCTCAAACAGAAAGAAAAGGAGGATC
AGGTGTTGTCCTACATCAATGGGTACAACAAGCAAACCTGGAGTATCCTGGTCTACTCC
ATGCCCTCCCGAACCTGTCCTGCGCTGGAGGGTCTCCAGGAGAAAGACTCTGGCCCTA
CAGCTGCTCCGTGAATGTGCAAGACAAACAAGCAAATCTAGGGCACAGCATAAAACCT
TAGAACTCAATGTACTGGTCTCCAGCTCCTCCATCCTGCCGTCTCCAGGGTGTGCCCAT
GTGGGGCAAACGTGACCCTGAGCTGCCAGTCTCCAAGGAGTAAGCCCGTGTCCAATACCA
GTGGGATCGGCAGCTCCATCCTCCAGACTTCTTGACCCAGCATTAGATGTATCCGTG
GGTCTTAAGCCTACCAACCTTCGTCTTCCATGGCTGGAGTCTATGTCTGCAAGGCCAC
AATGAGGTGGGCACTGCCAATGTAATGTGACGCTGGAAGTGAGCACAGGGCTGGAGCTGC
AGTGGTTGCTGGAGCTGTTGGTACCTGGTGGACTGGGTTGCTGGCTGGCTGGTCC
TCTTGTACCACCGCCGGCAAGGCCCTGGAGGAGCCAGCCAATGATATCAAGGAGGATGCC
ATTGCTCCCCGGACCCTGCCCTGGCCAAGAGCTCAGACACAATCTCCAAGAATGGGACCC
TTCCTCTGTACCTCCGCACGAGCCCTCCGGCCACCCATGGCCCTCCAGGCCTGGTGCAT
TGACCCCCACGCCAGTCTCCAGCCAGGCCCTGCCCTCACCAAGACTGCCACGACAGAT
GGGGCCCACCCCTCAACCAATATCCCCATCCCTGGTGGGTTCTCCTCTGGCTTGAGCCG
CATGGGTGCTGTGCCTGTGATGGTGCCTGCCAGAGTCAGCTGGCTCTGGTAT**GATGAC**
CCCACCACTATTGGCTAAAGGATTGGGTCTCTCCTCTATAAGGGTCACCTCTAGCAC
AGAGGCCTGAGTCATGGAAAGAGTCACACTCCTGACCCTAGTACTCTGCCACCTCTC
TTTACTGTGGAAAACCATTCTCAGTAAGACCTAAGTGTCCAGGAGACAGAAGGAGAAGAGGA
AGTGGATCTGGAATTGGAGGAGCCTCCACCCACCCCTGACTCCTCCTATGAAGGCCAGCTG
CTGAAATTAGCTACTCACCAAGAGTGAGGGCAGAGACTCCAGTCAGTGAGTCTCCAGGC
CCCCCTGATCTGTACCCACCCCTATCTAACACCACCCCTGGCTCCACTCCAGCTCCGT
ATTGATATAACCTGTCAGGCTGGCTGGTTAGGTTACTGGGCAGAGGATAGGAAATCTC
TTATTAAAACATGAAATATGTGTTCTGAAATTAAATAAGATACATAA
TGTTGTATGAAAAA

FIGURE 17

MISLPGPLVTNLLRFLFLGLSALAPPSRAQLQLHLPANRLQAVEGGEVVLPAWYTLHGEVSS
SQPWEVPFVMWFFKQKEKEDQVLSYINGVTTSKPGVSLVYSMPSRNLSLRLEGHQEKDSGPY
SCSVNVQDKQGKSRGHSIKTLELNVLVPPAPPSCRLQGVPHVGANVTLSCQSPRSKPAVQYQ
WDRQLPSFQTFFAPALDVIRGSLSTNLSSSMAGVYVCKAHNEVGTACQCNVTLEVSTGPGAA
VVAGAVVGTIVGLGLLAGLVLLYHRRGKALEEPANDIKAEDAIAPRTLWPWPKSSDTISKNGTL
SSVTSARALRPPHGPPRPGALTPTPSLSSQALPSPRLPTTDGAHPQPISPPIPGGVSSGLSR
MGAVPVMVPAQSQAGSLV

Signal peptide:

amino acids 1-29

Transmembrane domain:

amino acids 245-267

N-glycosylation site.

amino acids 108-112, 169-173, 213-217, 236-240, 307-311

N-myristoylation site.

amino acids 90-96, 167-173, 220-226, 231-237, 252-258, 256-262;
262-268, 308-314, 363-369, 364-370

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 164-175

FIGURE 18

CGCCACCACTGCGGCCACCGCCA**AT**GAAACGCCCTCCGCTCCTAGGGTTTTCCACTTTG
TTGAATTGTTCTATACTCAAATTGACCAAGACACCTTGTCTCCAAATGCAAATGTGA
AATACGCAATGGAATTGAGCCTGCTATTGCAACATGGGATTTCAGGAAATGGTGTACAA
TTTGTGAAGATGATAATGAATGTGGAAATTAACTCAGTCCTGTGGCGAAATGCTAATTGC
ACTAACACAGAAGGAAGTTATTATTGTATGTGTACCTGGCTTCAGATCCAGCAGTAACCA
AGACAGGTTTACTAATGATGGAACCGTCTGTATAGAAAATGTGAATGCAAACGTGCCATT
TAGATAATGTCTGTATAGCTGCAAATATTAATAAAACTTAAACAAAAATCAGATCCATAAAA
GAACCTGTGGCTTGCTACAAGAAGTCTATAGAAATTCTGTGACAGATCTTCACCAACAGA
TATAATTACATATAGAAATTAGCTGAATCATCTCATTACTAGGTACAAGAACAAACA
CTATCTCAGCCAAGGACACCCTTCTAACTCAACTCTTACTGAATTGTAACACCGTGAAT
AATTGTGTCAGGAGGATACATTGTAGTTGGACAAGTTATCTGTGAATCATAGGAGAAC
ACATCTTACAAAACATGCACACTGTTGAACAAGCTACTTTAAGGATATCCCAGAGCTTCC
AAAAGACCACAGAGTTGATACAAATTCAACGGATATAGCTCTCAAAGTTTCTTTGAT
TCATATAACATGAAACATATTCATCCTCATATGAATATGGATGGAGACTACATAAATATATT
TCCAAAGAGAAAAGCTGCATATGATTCAAATGGCAATGTTGCAGTGCATTTTATATTATA
AGAGTATTGGTCTTGCTTCATCATCTGACAACCTTATTGAAACCTCAAATTATGAT
AATTCTGAAGAGGAGGAAAGAGTCATATCTCAGTAATTCACTGAGCTCAAACCC
ACCCACATTATGAACCTGAAAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATA
GGTATAGGAGTCTATGTGCATTGGAAATTACTCACCTGATACCATGAATGGCAGCTGGTCT
TCAGAGGGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGTGTAATCACCT
GACACATTGCAATTGTGATGTCCTCTGGCCTTCCATTGGTATTAAGATTATAATATTCT
TTACAAGGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTC
ACCTCTGGTCTTCAGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTGCTG
TAGCCTATTGCTGAACTTGTGTTCTGTTGGATCAATACAAACTAATAAGCTCT
TCTGTTCAATCATGCCGACTGCTACACTACTTCTTTAGCTGTTTGATGGATGTGC
ATTGAAGGCATACATCTCATCTCATTGTTGGGTGTCACTACAAACAAGGGATTTGCA
CAAGAATTTTATATCTTGGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCAC
TAGGATACAGATATTATGGCACAAACCAAGTATGTTGGCTTAGCACCAGAAACAACCTTATT
TGGAGTTTATAGGACCAGCATGCCATTCTGTTAATCTTGGCTTGGAGTCAT
CATATACAAAGTTTCTGTCACACTGCAGGGTTGAAACCAAGAAGTTAGTGTGTTGAGAAC
TAAGGTCTGTGCAAGAGGAGCCCTCGCTCTGTTCTCGGCACCACCTGGATCTT
GGGTTCTCCATGTTGTGCACGCATCAGGGTTACAGCTTACCTCTCACAGTCAGCAATGC
TTTCCAGGGGATGTTCATTTTTATTCTGTGTTTATCTAGAAAGATTCAAGAAGAAT
ATTACAGATTGTCAAAATGTCCTGTTGGATGTTAAGG**TAA**ACATAGAGAAC
GTGGATAATTACAACGTGACAAAATAAAAATTCAAGCTGTGGATGACCAATGTATAAAA
TGACTCATCAAATTATCAATTAAACTACTAGACAAAAGTATTAAATCAGTTTCT
GTTTATGCTATAGGAACTGTAGATAATAAGGTTAAATTATGTATCATATAGATATACTATGT
TTTCTATGTGAAATAGTTCTGTCAAAATAGTATTGAGATATTGGAAAGTAATTGGTTT
CTCAGGAGTGTATCACTGCACCCAGGAAAGATTCTTCTAACACGAGAAGTATATGAA
TGTCTGAAAGGAAACCACTGGCTGATATTCTGTGACTCGTGTGCTTGAACACTAGTCC
CCTACCACTCGTAATGAGCTCATTACAGAAAGTGGAACATAAGAGAACAGGGCAGA
ATATCAAACAGTGAAGGAAATGATAAGATGTATTGAACTGAACTGTTTTCTGTAGAC
TAGCTGAGAAATTGTTGACATAAAATAAGAATTGAAGAACACATTACCTTACCTTGTGAA
TTGTTCTGAACTTAAATGTCCACTAAAACAACCTAGACTTCTGTTGCTAAATCTGTTCTT
TTCTAATATTCTAAAAAAAAAGGTTACCTCCACAAATTGAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAA

FIGURE 19

MKRLPLVVVFSTLLNCYTQNCTKTPCLPNAKEIRNGIEACYCNMGFSGNGVTICEDDNEC
GNLTQSCGENANCTNTEGSYYCMCVPGFRSSSNQDRFITNDGTVCIENVNANCHLDNVCIAA
NINKTLTKIRSIKEPVALLQEYVRNSVTDLSPTDIITYIEILAESSLLGYKNNTISAKDTL
SNSTLTFVKTVNNFVQRDTFVVWDKLSVNHRRTHTKLMHTVEQATLRIQSFFQKTTEFDT
NSTDIALKVFFFDSYNMKHIHPHMNMDGDYINIIFPKRKAAYDSNGNVAVAFLYYKSIGPLLS
SSDNFLLPQNYDNSEEEERVISSVISVSMSSNPPTLYELEKITFTLSRKVTDYRSLCAF
WNYSPDTMNGWSSEGCELYSNETHTSCRNCNLTHFAILMSGPSIGIKDYNILTRITQLG
IIISLICLAI CIFTFWFFSEIQSTRTTIHKNLCCSLFLAELVFLVGINTNTNKLFC SIIAGL
LHYFFLAFAFWMCIEGIHLYLIVVGVIYNKGFLHKNFYIFGYLSPA VVGFSAALGYRYGGT
TKVCWLSTENNFIWSFIGPACLIILVNLLAFGVIIYKVFRHTAGLKPEVSCFENIRSCARGA
LALLFLLGTTWIFGVVLHVHASVVTAYLFTVSNAFQGMFIFLFLCVLSRKIQEEYYRLFKNV
PCCFGCLR

Signal peptide:

amino acids 1-19

Transmembrane domain:

amino acids 430-450, 465-486, 499-513, 535-549, 573-593, 619-636,
648-664

N-glycosylation site.

amino acids 15-19, 21-25, 64-68, 74-78, 127-131, 177-181,
188-192, 249-253, 381-385, 395-399

Glycosaminoglycan attachment site.

amino acids 49-53

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 360-364

Casein kinase II phosphorylation site.

amino acids 54-58, 68-72, 76-80, 94-98, 135-139, 150-154,
155-159, 161-165, 181-185, 190-194, 244-248, 310-314, 325-329,
346-350, 608-612

Tyrosine kinase phosphorylation site.

amino acids 36-44, 669-677, 670-678

N-myristoylation site.

amino acids 38-44, 50-56, 52-58, 80-86, 382-388, 388-394,
434-440, 480-486, 521-527

Aspartic acid and asparagine hydroxylation site.

amino acids 75-87

FIGURE 20

TGGAAACATATCCTCCCTCATATGAATATGGATGGAGACTACATAAATATATTCCAAAGNG
AAAAGCCGGCATATGGATTCAAATGGAATGTTGCAGTCATTTATATTATAAGAGTAT
TGGTCCCTTGCTTCATCATCTGACAACCTCTTATTGAAACCTCAAAATTATGATAATTCT
GAAGAGGAGGAAAGAGTCATATCTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCAC
ATTATATGAACTTGAAAAATAACATTACATTAAGTCATCGAAAGGTACAGATAGGTATA
GGAGTCTATGTGGCATTTGGAATACTCACCTGATACCAGAATGGCAGCTGGTCTTCAGAG
GGCTGTGAGCTGACATACTCAAATGAGACCCACACCTCATGCCGCTGTAATCACCTGACACA
TTTGCAATTGATGTCCTCTGGCCTCATTGGTATTAAAGATTATAATATTCTTACAA
GGATCACTCAACTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTTACCTTC
TGGTTCTCAGTGAATTCAAAGCACCAGGA

FIGURE 21

GCTCCCAGCCAAGAACCTGGGGCCGCTGC CGGTGGGGAGGAGTCCCCGAAACCCGGCCG
CTAAGCGAGGCCTCCTCCCGCAGATCCGAACGGCTGGCGGGGTCAACCCGGCTGGGA
CAAGAACCGCCGCCGCTGCCTGCCCGGGGGAGGGCTGGGCTGGGCGGAGGCAG
GGTGTGAGTGGGTGTGCGGGGGGGAGGCTTGATGCAATCCGATAAGAAATGCTCGG
TGTCTGGCACCTACCGTGGGCCGTAAGCGCTACTATATAAGGCTGCCGGGGAG
CCGCCGCCGCGTCAGAGCAGGAGCGCTCGTCAGGATCTAGGCCACGACCATCCAACCC
GGCACTCACAGCCCCCAGGCCATCCGGTCGCCAGCCTCCGACCCCCATGCCGG
AGCTGCAGGAGAGCCCCAGGGAGGTGCCATGCCGGAGCGGGTGTGTTGGTCCACGTATGG
ATCCTGGCCGGCCTGGCTGGCGTGGCCGGCGCCCCCTCGCCTCTCGGACGCCGG
CCACGTGCACTACGGCTGGCGACCCCATCCGCTGCCGACCTGTACACCTCCGGCCCC
ACGGGCTTCCAGCTGCTTCTGCCATCCGTGCCAGGGCTGGACTGCCGGGG
CAGAGCGGCACAGTTGCTGGAGATCAAGGAGTCAGCTGCTCTGCCGACCGTGGACTCAAGGG
CGTGCACAGCGTGGGTACCTCTGCATGGCGCCAGGGCAAGATGCAAGGGCTGTTCAAGGG
ACTCGGAGGAAGACTGTGCTTCTGAGGAGGAGATCCGCCAGATGGCTACAATGTGACCGA
TCCGAGAACGCCCTCCGGTCTCCCTGAGCAGTGCCAACAGCGGAGCTGTACAAGAA
CAGAGGCTTCTCACTCTCATTCTGCCATGCTGCCATGGTCCCAGAGGAGCCTG
AGGACCTCAGGGGCCACTTGAATCTGACATGTTCTGCCCTGGAGACCGACAGCATG
GACCCATTGGCTGTGACCGGACTGGAGGGCGTGAGGAGTCCAGCTTGAGAAGTAACT
GAGACCATGCCGGCCTTCACTGCTGCCAGGGCTGTGGTACCTGCAGCGTGGGGACG
TGCTCTAGAACAGTCCAGTCCAGTCTGTTAGCTTAGGAAGAAACATCTAGAA
GTGTACATATTCAAGAGTTCCATTGGCAGTGCAGTTCTAGCCAATAGACTGTCTGAT
CATAACATTGTAAGCTGTAGCTGCCAGCTGCTGCCAGGGCCCCATTCTGCCCTCGA
GGTTGCTGGACAAGCTGCTGCACTGCTCAGTTCTGCTGAATACCTCCATCGATGGGAAC
TCACCTCCTTGGAAAATTCTTATGTCAGCTGAAATTCTCTAATTTCATCACTTC
CCCAGGAGCAGCCAGAACAGACAGGAGTAGTTAATTCAAGAACAGGTGATCCACTCTGTA
AAACAGCAGGTAAATTCACTCAACCCATGTTGAAATTGATCTATCTCTACTCCAGGG
ACCATTGCCCTCCCAAATCCCTCCAGGCCAGAACTGACTGGAGCAGGCATGCCACCAG
GCTTCAGGAGTAGGGGAAGCCTGGAGCCCCACTCCAGCCCTGGGACAACCTGAGAATTCCCC
CTGAGGCCAGTTCTGTCATGGATGCTGCTGAGAATAACTTGCTGTCCGGTGTACCTGC
TTCCATCTCCAGGCCACCGCCCTGCCACCTCACATGCCCTCCCATGGATTGGGGCCT
CCCAGGCCCTCCAGCTTATGTCACCTGCACCTCTGTTCAAAATCAGGAAAAGAAAAGAT
TTGAAGACCCCAAGTCTGCAATAACTTGCTGTGGAAGCAGCGGGGAAGACCTAGAAC
CCTTCCCCAGCACTGGTTTCCAACATGATATTATGAGTAATTATTTGATATGTACA
TCTCTTATTCTTACATTATTATGCCCTAAATTATTTATGTATGTAAGTGAGGTTG
TTTGATATTAAATGGAGTTGTTGT

FIGURE 22

MRSGCVVHVWILAGLWLAVAGRPLAFSDAGPHVHYGWDPIRLHLYTSGPHGLSSCFLRI
RADGVVDCARGQSAHSLLIEIKAVALRTVAIKGVHSVRYLCMGADGKMQGLLQYSEEDCAFEED
EIRPDGYNVYRSEKHRLPVSLSSAKQRQLYKNRGFLPLSHFLPMLPMVPEEPEDLRGHLESD
MFSSPLETDSDMPFGLVTGLEAVRSPSFEK

Signal peptide:

amino acids 1-22

Casein kinase II phosphorylation site.

amino acids 78-82, 116-120, 190-194, 204-208

N-myristoylation site.

amino acids 15-21, 54-60, 66-72, 201-207

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 48-59

TOP SECRET//NOFORN

FIGURE 23

CCCAGAAGTTCAAGGGCCCCGGCCTCCTGCCTCGCCGCCGGACCCCTGACCTCCTCA
GAGCAGCCGGCTGCCGCCCCGGAAAGATGGCGAGGAGGAGCCGCCACCGCCTCCTGCTG
CTGCTGCCTACCTGGTGGTCGCCCTGGCTATCATAAGGCCTATGGGTTTCTGCCAAA
AGACCAACAAGTAGTCACAGCAGTAGAGTACCAAGAGGCTATTTAGCCTGAAAACCCAA
AGAAGACTGTTCCAGATTAGAGTGGAGAAACTGGGTGGAGTGCTCCTTGTCTAC
TATCAACAGACTCTCAAGGTGATTTAAAAATCGAGCTGAGATGATAGATTCAATATCCG
GATCAAAAATGTGACAAGAAGTGTGAGCTGGGGAAATATCGTTGTGAAGTTAGTGCCTCATCTG
AGCAAGGCCAAACCTGGAAGAGGATACAGTCAGTCTGGAAAGTATTAGTGGCTCCAGCAGTT
CCATCATGTGAAGTACCCCTCTGCTCTGAGTGGAACTGTGGTAGAGCTACGATGTCAAGA
CAAAGAAGGAAATCCAGCTCTGAATAACACATGGTTAACCGATGGCATCCGTTGCTAGAAA
ATCCCAGACTGGCTCCAAAGCACCAACAGCTCATACACAATGAATAACAAAACGGAACT
CTGCAATTAAACTGTTCCAAACTGGACACTGGAGAAATATTCCGTGAAGCCCGCAATT
TGTTGGATATCGCAGGTGTCCCTGGAAACGAATGCAAGTAGATGATCTAACATAAGTGGCA
TCATAGCAGCCGTAGTAGTTGTGGCCTAGTGATTTCCGTTGTGGCCTGGTATGCTAT
GCTCAGAGGAAAGGCTACTTTCAAAAGAAACCTCTTCCAGAACAGTAATTCTCATCTAA
AGCCACGACAATGAGTGGAAATGTGCAGTGGCTCACGCCGTAAATCCCAGCACTTGGAGG
CCGGCGGGCGGATCACGAGGTCAAGGAGTTCTAGACCAGTCTGGCAATATGGTGAACACCC
CATCTCTACTAAAATACAAAAATTAGCTGGCATGGTGGCATGTGCCTGCAGTTCCAGCTGC
TTGGGAGACAGGAGAAATCACTGAACCCGGGAGGCAGGTTGCAGTGAGCTGAGATCACCG
CACTGCAGTCCAGCCTGGTAACAGAGCAAGATTCCATCTCAAAAATAAAATAATA
AATAAAATACTGGTTTACCTGTAGAATTCTTACAATAATAGCTTGATATT

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FIGURE 24

MARRSRHRLLLLLLRYLVVALGYHKAYGFSAPKQQVVTAVEYQEAILACKTPKKT
WKKLGRSVSFVYYQQTLQGDFKNRAEMIDFNIRIKNVTRSDAGKYRCEVSAPSEQQNLEED
TVTLEVLVAPAVPSCEVPSSALSGTVVELRCQDKEGNPAPEYTWFKDGI
RLLENPRLGSQST
NSSYTMNTKTGTLQFNTVSKLDTGEYSCEARN
SVGYRRCPGKRMQVDDLNISGIIAAVVVA
LVI
SVCGLGV
CYAQRKG
YFSKETSFQKS
N
SSSKATTMSE
NVQWL
TPV
IPALWKA
AAAGGSRG
QEF

Signal peptide:

amino acids 1-20

Transmembrane domain:

amino acids 130-144, 238-258

N-glycosylation site.

amino acids 98-102, 187-191, 236-240, 277-281

Casein kinase II phosphorylation site.

amino acids 39-43, 59-63, 100-104, 149-153, 205-209, 284-288

N-myristoylation site.

amino acids 182-188, 239-245, 255-261, 257-263, 305-311

Amidation site.

amino acids 226-230

FIGURE 25

GACATCGGAGGTGGCTAGCACTGAAACTGCTTTCAAGACGAGGAAGAGGAGGAGAAAGAG
AAAGAAGAGGAAGATGTTGGCAACATTATTAACTGCTCCACAGCCGGACCCCTGGCAT
CATGCTGCTATTCTGCAAATACTGAAGAAGCATGGGATTAAATATTACTTCTAAATAA
ATGAATTACTCAATCTCCTATGACCACCTACATACATACTCCACCTCAAAAAGTACATCAATA
TTATATCATTAGGAAATAGTAACCTTCTCCAAATATGCATGACATTGGACAAATG
CAATTGTGGCACTGGCACTTATTCAGTGAAGAAAAACTTGTGGTTCTATGGCATTATCA
TTTGACAAATGCAAGCATCTCCTTATCAATCAGCTCCTATTGAACTTACTGACTGACTG
TGGAACTCTTAAGGGCCATTACATTCTGAAGAAGAAAGCTAAGATGAAGGACATGCCACT
CCGAATTCTATGTGCTACTTGGCCTAGCTATCACTACACTAGTACAAGCTGTAGATAAAAAAG
TGGATTGTCCACGGTTATGTACGTGTAAATCAGGCCTGGTTACACCCAGATCCATTAT
ATGGAAGCATCTACAGTGGATTGTAATGATTAGGTCTTTAACCTTCCAGCCAGATTGCC
AGCTAACACACAGATTCTCCTACAGACTAACAAATTGCAAAATTGAATACTCCACAG
ACTTTCCAGTAAACCTACTGGCCTGGATTATCTCAAAACAATTATCTCAGTCACCAAT
ATTAATGTAAGGAAAGATGCCTCAGCTCCTTCTGTGTACCTAGAGGAAACAAACTACTGA
ACTGCCTGAAAATGCTGTCGAAGTCAAGCACTTACAAGAACTCTATATTAACTACA
TGCTTCTACAATTTCACCTGGAGCCTTATTGGCCTACATAATCTCTCGACTTCATCTC
AATTCAAATAGATTGCAGATGATCAACAGTAAGTGGTTGATGCTCTCAAATCTAGAGAT
TCTGATGATTGGGAAATCCAATTATCAGAAATCAAAGACATGAACATTAAAGCCTCTTATCA
ATCTTCGAGCCTGGTTATAGCTGGTATAAACCTCACAGAAATACCAGATAACGCCCTGGTT
GGACTGGAAAACCTAGAAAGCATCTCTTTACGATAACAGGGTTATTAAAGTACCCCATGT
TGCTCTCAAAAGTTGTAATCTCAAATTGGATCTAAATAAAATCTATTAAAGAA
TACGAAGGGGTGATTAGCAATATGCTACACTAAAGAGTTGGGATAAAATAATATGCCT
GAGCTGATTCCATCGATAGTCTGCTGTGGATAACCTGCCAGATTAAAGAAAAATAGAAGC
TACTAACACCTAGATTGTCTTACATTCAACCCAAATGCATTTCAGACTCCCCAAGCTGG
AATCACTCATGCTGAACAGCAATGCTCTCAGTGCCTGTACCATGGTACATTGAGTCTCTG
CCAAACCTCAAGGAAATCAGCATACACAGTAACCCCATCAGGTGTGACTGTGATCCGTTG
GATGAACATGAACAAAACCAACATTGAGTCACTGGAGCCAGATTCACTGTTTGCCTGGACC
CACCTGAATTCCAAGGTCAAATGTTGGCAAGTGCATTCAAGGACATGATGGAAATTGT
CTCCCTCTTATAGCTCCTGAGAGCTTCCCTAATCTAAATGTTAGAAGCTGGAGCTATGT
TTCCCTTCAGTGTAGAGCTACTGCAGAACACCACAGCCTGAAATCTACTGGATAACACCTCTG
GTCAAAACTCTGCCTAATACCCCTGACAGACAAGTTCTATGTCCATTCTGAGGGAAACACTA
GATATAATGGCGTAACTCCCCAAAGAAGGGGGTTATATACTTGTATAGCAACTAACCTAGT
TGGCGCTGACTTGAAGTCTGTTATGATCAAAGTGGATGGTCTTCCACAAGATAACAATG
GCTCTTGAATATTAAAATAAGAGATATTCAAGGCCATTCAAGTTGGTGTCTGGAAAGCA
AGTTCTAAATTCTCAAATCTAGTGTAAATGGACAGCCTTGTCAAGACTGAAATTCTCA
TGCTGCGCAAAGTGCCTGAATACCATCTGATGTCAAGGTATATACTTACTCATCTGAATC
CATCAACTGAGTATAAAATTGTATTGATATTCCCACCATCTATCAGAAAAACAGAAAAAAA
TGTGTAATGTCACCACCAAGGTTGCACCCCTGATCAAAGAGTATGAAAAGAATAATAC
CACAAACACTTATGGCCTGTCTGGAGGCCTCTGGGGATTATTGGTGTGATATGTCTTATCA
GCTGCCTCTCCAGAAATGAACTGTGATGGTGGACACAGCTATGTGAGGAATTACTTACAG
AAACCAACCTTGCATTAGGTGAGCTTATCCTCTGATAAAATCTGGGAAGCAGGAAA
AGAAAAAAAGTACATCACTGAAAGTAAAGCAACTGTTAGGTTACCAACAAATATGTCC
AAAAACCAAGGAAACCTACTCCAAAATGAAC

FIGURE 26

MKDMPLRIHVLLGLAITTLVQAVDKVDCPRLCTCEIRPWFTPRSIYMEASTVDCNDLGLLT
FPARLPANTQILLQTNNAKIEYSTDFPVNLTGLDLSQNNLSSVTNINVKKMPQLLSVYLE
ENKLTELPEKCLSELNLQELYINHNLLSTISPGAFIGLHNLLRLHNSNRLQMINSKWFDA
LPNLEILMIGENPIIRIKDMNFKPLINLRSVIAGINLTEIPDNALVGLENLESISFYDNRL
IKVPHVALQKVNLKFIDLNKNPINRIRRGDFSNMLHLKELGINNMPELISIDSLAVDNLPD
LRKIEATNNPRLSYIHPNAFFRLPKLESMLNSNALSAHYGTIESLPNLKEISIHSNPIRC
DCVIRWMNMNKTNIRFMEPDSLFCVDPPFEQGQNVRQVHFRDMMEICLPLIAPESFPSNLNV
EAGSYVSFHCRTAEPQPEIYWITPSGQKLLPNTLTDKFYVHSEGTLDINGVTPKEGGLYTC
IATNLVGAIDLKSVMIKVDGSFPQDNNGSLNIKIRDIQANSVLVSWKASSKILKSSVKWTAFV
KTENSAAQSARI PSDVKVYNLTHLPSTEYKICIDIPTIYQKNRKKCVNVTKGHLHPDQKE
YEKNNTTLMACLGGLGIIGVICLISCLSPEMCDGGHSYVRNYLQKPTFALGELYPPLIN
LWEAGKEKSTSLKVATVIGLPTNMS

Signal sequence:

amino acids 1-22

Transmembrane domain:

amino acids 633-650

N-glycosylation site.

amino acids 93-97, 103-107, 223-227, 382-386, 522-526, 579-583,
608-612, 624-628, 625-629

Casein kinase II phosphorylation site.

amino acids 51-55, 95-99, 242-246, 468-472, 487-491

Tyrosine kinase phosphorylation site.

amino acids 570-579

N-myristoylation site.

amino acids 13-19, 96-102, 158-164, 221-227, 352-358, 437-443,
491-497, 492-498, 634-640, 702-708

Cell attachment sequence.

amino acids 277-280

FIGURE 27

FLOWERS

GCCCGGGACTGGCGCAAGGTGCCAAGCAAGGAAAGAAATAATGAAGAGACACATGTGTTAG
CTGCAGCCTTTGAAACACGCAAGAAGGAAATCAATAGTGTGGACAGGGCTGGAACCTTAC
CACGCTTGTGGAGTAGATGAGGAATGGGCTCGTATTATGCTGACATTCCAGCATGAATCT
GGTAGACCTGTGGTTAACCGTTCCCTCTCCATGTGTCTCCTCCTACAAAGTTGTTCTTA
TGATACTGTGCTTCATTCTGCCAGTATGTGTCCCAAGGGCTGTCTTGTCTCCTCTGGG
GGTTAAATGTCACCTGTAGCAATGCAAATCTCAAGGAAATACCTAGAGATCTCCTCCTGA
AACAGTCTTACTGTATCTGGACTCCAATCAGATCACATCTATTCCAATGAAATTAAAGG
ACCTCCATCAAACTGAGAGTTCTAACCTGTCCAAAAATGGCATTGAGTTATCGATGAGCAT
GCCTCAAAGGAGTAGCTGAAACCTTGCAGACTCTGGACTTGTCCGACAATCGGATTCAAAG
TGTGCACAAAAATGCCCTCAATAACCTGAAGGCCAGGGCCAGAATTGCCAACAAACCCCTGGC
ACTGCGACTGTACTCTACAGCAAGTTCTGAGGAGCATGGCGTCCAATCATGAGACAGCCCAC
AACGTGATCTGTAAAACGTCCGTGTTGGATGAACATGCTGGCAGACCATTCTCAATGCTGC
CAACGACGCTGACCTTGTAACCTCCCTAAAAAAACTACCGATTATGCCATGCTGGTCACCA
TGTGCTGGCTGTTCACTATGGTATCTCATATGTTGATATTATGTGAGGCAAATCAGGAG
GATGCCGGAGACACCTCGAATAACTTGAAATCCCTGCCAAGCAGGCAGAAGAAAGCAGATGA
ACCTGATGATATTAGCACTGTGGTAAGTGTCCAAACTGACTGTCATTGAGAAAGAAAGAAA
GTAGTTGCGATTGCAGTAGAAATAAGTGGTTACTTCTCCATCCATTGAAACATTTGAA
ACTTTGTATTCAGTTTTGAATTATGCCACTGCTGAACTTTAACAAACACTACAACA
TAAATAATTGAGTTAGGTGATCCACCCCTTAATTGTACCCCCGATGGTATATTCTGAGT
AAGCTACTATCTGAACATTAGTTAGATCCATCTCACTATTAAATAATGAAATTATTTTTT
AATTAAAAGCAAATAAAAGCTTAACTTGAACCAGGGAAAAAAAAAAAAAAACA

FIGURE 28

MNLVDLWLTRSLSMCLLLQSFVLMILCFHSASMC PKGCLCSSGGLNVTCSNANLKEIPRDL
PPETVLLYLDQNQITSIPNEIFKDLHQLRVLNLSKNGIEFIDEHAFKGVAETLQTLDLSDNR
IQSVHKNAFFNNLKARARIANNPWHCDCTLQQVLRSMASNHETAHNVICKTSVLDEHAGRPFL
NAANDADLCNLPKKTTDYAMLVTMFGWFTMVISYVVYYVRQNQEDARRHLEYLKSLPSRQKK
ADEPDDISTVV

Signal sequence:

amino acids 1-33

Transmembrane domain:

amino acids 205-220

N-glycosylation site.

amino acids 47-51, 94-98

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 199-203

Casein kinase II phosphorylation site.

amino acids 162-166, 175-179

N-myristoylation site.

amino acids 37-43, 45-51, 110-116

FIGURE 29

ACCGAGCCGAGCGGACCGAAGGCAGCAGGTGAGCAAGAGGATGCTGGCGGG
GGCGTGAGGAGCATGCCAGCCCCCTCTGGCCTGCTGGCAGCCCACCTCCTGCTGGTGCT
GGGCTCAGTGTGTCAGGCTGGCACGGCTGCCGCCGCTGCGAGTGCTCCGCCAGG
ACCGCGCTGTGCTGTGCCACCGCAAGTGCTTGAGCTGGCAGTCCCCGAGGGCATCCCCACCGAG
ACCGCCTGCTGGACCTAGGCAAGAACCGCATCAAACGCTAACCGAGCAGGACGAGTTGCCAG
CTTCCGACCTGGAGGAGCTGGAGCTAACGAGAACATCGTGAGCGCCGTGGAGGCCGG
CCTCAACAACCTCTAACCTCCGACGCTGGCTCCGCAGCAACGCCGCTGAAGCTCATC
CCGCTAGGCGTCTTCACTGGCTCAGAACCTGACCAAGCAGGACATCAGCGAGAACAGAT
CGTTATCCTACTGGACTACATGTTCAGGACCTGTACAACCTCAAGTCAGTCACTGGAGGTTGGCG
ACAATGACCTCGTCTACATCTCACCGCCTCAGGGCCTAACAGCCTGGAGCAGCTG
ACGCTGGAGAAATGCAACCTGACCTCATCCCCACCGAGGCGTGTCCCACCTGCACGGCCT
CATCGTCTGGAGGCTCCGGCACCTAACATCAATGCCATCGGGACTACTCCTTCAAGAGGC
TGTACCGACTCAAGGTCTGGAGATCTCCACTGGCCTACTGGACACCATGACACCCAAC
TGCCTCTACGGCCTAACCTGACGTCCCTGTCCATCACACACTGCAATCTGACCGCTGTGCC
CTACCTGGCCGTCCGCCACCTAGTCTATCTCCGCTTCTCAACCTCTCCTACAACCCCCATCA
GCACCATTGAGGGCTCCATGTTGCATGAGCTGCTCCGGCTGCAGGAGATCCAGCTGGTGGC
GGCAGCTGGCGTGGTGGAGCCCTATGCCTTCCGGCCTCAACTACCTGCGCGTGTCAA
TGTCTCTGGCAACCAAGCTGACCAACTGGAGGAATCAGTCTTCACTCGGTGGCAACCTGG
AGACACTCATCTGGACTCCAACCCGCTGGCTGCGACTGTCGGCTCTGTGGTGTCCGG
CGCCGCTGGGGCTCAACTAACCGGCAGCAGCCCACGTGCGCCACGCCAGTGGTGTCCA
GGGCAAGGAGTTCAAGGACTTCCCTGATGTGCTACTGCCAACTACTCACCTGCCGCCGCG
CCCGCATCCGGACCGCAAGGCCAGCAGGTGTTGTGGACGAGGCCACCGTGCAGTT
GTGTGCCGGCCGATGGCGACCCGCCGCCATCCTCTGGCTCTCACCCGAAAGCACCT
GGTCTCAGCCAAGAGCAATGGCGGCTCACAGTCTCCCTGATGGCACGCTGGAGGTGCGCT
ACGCCAGGTACAGGACAACGGCACGTACCTGTGCATCGCGCCAACGCCGGCAACGAC
TCCATGCCGCCACCTGCATGTGCAGCTACTGCCACTGGCCCCATGCCAACAA
GACCTTCGCTTCATCTCAACCAGCCGGCAGGGAGAGGCCAACAGCACCCGCCACTG
TGCCTTCCCTCGACATCAAGACCCTCATCATGCCACCACATGGCTTCATCTCTTC
CTGGCGTCGTCCTCTGCCTGGTGTGCTGTTCTCTGGAGGCCGGCAAGGGCAACAC
AAAGCACAAACATCGAGATCGAGTATGTGCCCGAAAGTCGGACCGAGGCATCAGCTCCGCCG
ACGGCCCCGCAAGTCAACATGAAGATGATATGAGGCGGGGGGGGGCAGGGACCCCCG
GGCGGCCGGCAGGGGAAGGGCCTGGTCGCCACCTGCTCACTCTCCAGTCTCCACCT
CTCCCTACCTCTACACACGTTCTTTCTCCCTCCGCCCTCGTCCCTGCTGCCCG
CCAGCCCTCACCACTGCCCTCTACCGACCTCAGAAGCCCAGACCTGGGGACCCCA
CCTACACAGGGGCATTGACAGACTGGAGTTGAAAGCCGACGAACCGACACGCCAGAGTCA
ATAATTCAATAAAAAGTTACGAACCTCTGTAACTTGGTTCAATAATTATGGATTT
TATGAAAATTGAAATAATAAAAAGAGAAAAAAACTAAAAAAAAAAAAAA

FIGURE 30

MQVSKRMLAGGVRSMPSPLLACWQPI~~LLVLGSVLSGSATGCPRCECSAQDRAVLCHRKCF~~
VAVPEGIPTETRLLDGKNRIKTLNQDEFASFPHLEELENENIVSAVEPGAFNNLFNLRTL
GLRSNRKL~~IPLGVFTGLSNLTQDISENKIVILLDYMFDLYNLKSLEVGDNDLVYISHRA~~
FSGLNSLEQLTLEKCNLTSIPTEALSHLHGLIVRLRHLNINAIRDYSFKRLYRLKVLEISH
WPYLDTMTPNCLYGLNLTSLSITHCNLTAVPYLAVRHLVYLRFLNLSYNPISTIEGSMLHEL
LRLQEIQLVGGQLAVVEPYAFRGLNYLRVLNVSGNQLTTLEESVFHSVGNLETLLDSNPLA
CDCRLLWVFR~~RRWRNLNFNRQQPTCATPEFVQGKEFKDFPDVLLPNYFTCRRARIRDRKAQQV~~
FVDEGHTVQFVCRADGDP~~PPAILWLSPRKHLVSAKSNGRLTVFPDGTL~~EVRYAQVQDNGTYL
CIAANAGGND~~SMPAHLHVRSYSPDWPHQPNKTFAFISNQPGE~~GEANSTRATVPFPFDIKTLI
IATTM~~G~~FISFLGVVLFC~~L~~VLLFLWSRGKGNTKH~~NIEIEYVPRKSDAGISSADAPRKFNMKMI~~

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 556-578

N-glycosylation site.

amino acids 144-148, 202-206, 264-268, 274-278, 293-297, 341-345,
492-496, 505-509, 526-530, 542-546

Casein kinase II phosphorylation site.

amino acids 49-53, 108-112, 146-150, 300-304, 348-352, 349-353,
607-611

Tyrosine kinase phosphorylation site.

amino acids 590-598

N-myristoylation site.

amino acids 10-16, 32-38, 37-43, 113-119, 125-131, 137-143,
262-268, 320-326, 344-350, 359-365, 493-499, 503-509, 605-611

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 32-43

FIGURE 31

CCCCACCGCGTCCGCACCTCGGCCCGGGCTCCGAAGCGGCTCGGGGCGCCCTTCGGTCAAC
ATCGTAGTCCACCCCTCCCCATCCCCAGCCCCGGGATTCAAGGCTCGCCAGGCCAGCC
AGGGAGCCGGCCGGGAAGCGCG**AT**GGGGCCCCAGCCGCTCGCTCCTGCTCCTGCTCCTGC
TGTTCGCCTGCTGCTGGCGCCGGCGGGCCAACCTCTCCCAGGACGACAGCCAGCCCTGG
ACATCTGATGAAACAGTGGTGGCTGGTGGCACCGTGGCTCAAGTGCCAAGTGAAAGATCA
CGAGGACTCATCCCTGCAATGGCTAACCCCTGCTCAGCAGACTCTACTTGGGGAGAAGA
GAGCCCTTCGAGATAATCGAATTCAAGCTGGTTACCTCTACGCCAACAGAGCTCAGCATCAGC
ATCAGCAATGTGGCCCTGGCAGACGAGGGCGAGTACACCTGCTCAATCTTCACTATGCCTGT
GCGAACTGCCAAGTCCCTCGTCACTGTGCTAGGAATTCCACAGAACGCCATCATCACTGGTT
ATAAAATCTTCATTACGGGAAAAAGACACAGCCACCCCTAAACTGTCAGTCTTCTGGGAGCAAG
CCTGCAGCCCCGGCTCACCTGGAGAAAGGGTGACCAAGAACTCCACGGAGAACCAACCGCAT
ACAGGAAGATCCAATGGTAAAACCTTCACTGTCAGCAGCTCGGTGACATTCCAGGTTACCC
GGGAGGATGATGGGGCGAGCATCGTGTGCTCTGTGAACCATGAATCTCTAAAGGGAGCTGAC
AGATCCACCTCTCAACGCATTGAAGTTTATACACACCAACTGCGATGATTAGGCCAGACCC
TCCCCATCCTCGTGAGGGCCAGAACAGCTGTTGCTACACTGTGAGGGTCGCCAATCCAGTCC
CCCAGCAGTACCTATGGGAGAACGGAGGGCAGTGTGCCACCCCTGAAGATGACCCAGGAGAGT
GCCCTGATCTCCCTTCCTCAACAAGAGTGACAGTGGCACCTACGGCTGCACAGCCACCAAG
CAACATGGGCAGCTACAAGGCCTACTACACCCCTCAATGTTAATGACCCAGTCCGGTGCCT
CCTCCCTCCAGCACCTACCACGCCATCATCGTGGATCGTGGCTTCATTGTCTCCTGCTG
CTCATCATGCTCATCTCCCTGGCCACTACTTGATCCGGCACAAAGGAACCTACCTGACACA
TGAGGCAAAAGGCTCCGACGATGCTCAGACGGGACACGGCCATCATCAATGCAGAAGGCG
GGCAGTCAGGAGGGACGACAAGAAGGAATATTCAT**C**T**A**GAGGCGCTGCCACTTCCTGC
GCCCCCCAGGGCCCTGTGGGACTGCTGGGCCGTACCAACCCGGACTTGTACAGAGCAA
CCGCAGGGCCGCCCTCCGCTTGCTCCCCAGCCCACCCACCCCGTACAGAATGTCTGC
TTTGGGTGCGGTTTGACTCGGTTGGAATGGGGAGGGAGGGAGGGCGGGGGAGGGAGGG
TTGCCCTCAGCCCTTCCGTGGCTCTGCATTGGTTATTATTATTTGTAACAATCC
CAAATCAAATCTGTCTCCAGGCTGGAGAGGCAGGAGCCCTGGGTGAGAAAAGCAAAAAACA
AACAAAAAAACA

FIGURE 32

MGAPAASLLLLLFFACCWAPGGANLSQDDSQWPWTSDETVVAGGTVVLCQVKDHEDSSLQW
SNPAQQTLYFGEKRALRDNRQLVTSTPHELYSISISNVALADEGEYTCISIFTMPVRTAKSLV
TVLGIPQKPIITGYKSSLREKDTATLNCQSSGSKPAARLTWRKGDQELHGEPTRIQEDPNKG
TFTVSSSVTFQVTREDDGASIVCSVNHESLKGADRSTSQRIEVLYTPTAMIRPDPPHPREGQ
KLLLHCEGRGNPVPQQYLWEKEGSVPPLKMTQESALIFPFLNKSDSGTYGCTATSNMGSYKA
YYTLNVNDPSPVPSSSSTYHAIIGGIVAFIVFLLIMLIFLGHYLIRHKGTYLTHEAKGSDD
APDADTAIINAEGGQSGGDDKKEYFI

Signal sequence:

amino acids 1-20

Transmembrane domain:

amino acids 331-352

N-glycosylation site.

amino acids 25-29, 290-294

Casein kinase II phosphorylation site.

amino acids 27-31, 35-39, 89-93, 141-145, 199-203, 388-392

N-myristoylation site.

amino acids 2-8, 23-29, 156-162, 218-224, 295-301, 298-304,
306-310, 334-340, 360-364, 385-389, 386-390

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 33

GGGGGTTAGGGAGGAAGGAATCCACCCCCACCCCCCAAACCCCTTCTCCTTCCTGG
CTTCGGACATTGGAGCACTAAATGAACCTGAATTGTGTCTGTGGCGAGCAGGATGGTCGCTG
TTACTTTGTGATGAGATCGGGGATGAATTGCTCGCTTAAAAATGGCTTGGATTCTGTT
GCTGGAGACGTCTCTTGTGCTGGAAACGTTACAGGGACGTTGCAAAGAGAAGA
TCTGTTCTGCAATGAGATAGAAGGGGACCTACACGTAGACTGTGAAAAAAAAGGGCTTCACA
AGTCTGCAGCGTTCACTGCCCGACTTCCCAGTTTACCATTTATTCATGGCAATT
CCTCACTCGACTTTCCATAATGAGTCGCTAACCTTATAATGCGGTTAGTTGCACATGG
AAAACAATGGCTGATGAAATCGTCCGGGGCTTTCTGGGGCTGCAGCTGGTAAAAGG
CTGCACATCAACAAACAAGATCAAGTCTTCTGAAAGCAGACTTTCTGGGGCTGGACGA
TCTGGAATATCTCCAGGCTGATTTAATTATTACGAGATATAAGACCCGGGGCTTCCAGG
ACTTGAACAAGCTGGAGGTGCTCATTAAATGACAATCTCATCAGCACCCCTACCTGCCAAC
GTGTTCCAGTATGTGCCATACCCACCTCGACCTCCGGGTAACAGGCTGAAAACGCTGCC
CTATGAGGAGGTCTGGAGCAAATCCCTGGTATTGCGGAGATCCTGCTAGAGGATAACCCT
GGGACTGCACCTGTGATCTGCTCTCCCTGAAAGAATGGCTGGAAAACATTCCAAGAATGCC
CTGATCGGCCAGTGGTCTGCGAAGCCCCACAGACTGCAGGGTAAAGACCTCAATGAAAC
CACCGAACAGGACTTGTGTCCTTGAAAAACCGAGTGGATTCTAGTCTCCGGCGCCCCCTG
CCAAGAACAGAGACCTTGCTCCCTGGACCCCTGCCAACTCCTTCAAGACAAATGGCAAGAG
GATCATGCCACACCAGGGTCTGCTCCAAACGGAGGTACAAAGATCCCAGGCAACTGGCAGAT
CAAATCAGACCCACAGCAGCGATAGCGACGGTAGCTCCAGGAACAAACCTTAGCTAAC
GTTTACCCCTGCCCTGGGGCTGAGCTGCGACACATCCCAGGGTGGTTAAAGATGAAC
TGCAACAACAGGAACGTGAGCAGCTGGCTGATTTGAAGCCAAGCTCTAACGTGCAGGA
GCTTTCTACGAGATAACAAAGATCCACAGCATCGAAAATCGACTTTGTGGATTACAAGA
ACCTCATTCTGTTGGATCTGGCAACAATAACATCGCTACTGTAGAGAACAAACACTTCAAG
AACCTTTGGACCTCAGGTGGCTATACATGGATAGCAATTACCTGGACACGCTGTCCGGGA
GAAATTGCGGGGCTGCAAAACCTAGAGTACCTGAACGTGGAGTACAACGCTATCCAGCTCA
TCCTCCGGGCACTTCAATGCCATGCCAAACTGAGGATCCTCATTCTAACAAACAACCTG
CTGAGGTCCCTGCCTGTGGACGTGTTCGCTGGGTCTCGCTCTAAACTCAGCCTGCACAA
CAATTACTCATGTACCTCCGGTGGCAGGGTGCTGGACCAGTTAACCTCCATCATCCAGA
TAGACCTCCACGGAAACCCCTGGGAGTGCTCCTGCACAATTGTGCCCTTAAGCAGTGGGCA
GAACGCTGGGTTCCGAAGTGCTGATGAGCGACCTCAAGTGTGAGACGCCGGTGAACCTT
TAGAAAGGATTTCATGCTCCTCTCCAATGACGAGATCTGCCCTCAGCTGTACGCTAGGATCT
CGCCCACGTTAACCTCGCACAGTAAAACAGCACTGGGTTGGGGAGACCGGACGCACTCC
AACTCCTACCTAGACACCAGCAGGGTGTCCATCTGGTGTGGTCCGGACTGCTGCTGGT
GTTTGTACCTCCGCCCTCACCGTGGGGCATGCTCGTTATCCTGAGGAACCGAAAGC
GGTCCAAGAGACGAGATGCCAACCTCCCGTCCGAGATTAAATTCCCTACAGACAGTCTGT
GAECTTCCACTGGACAATGGCCTTACAACGCACTGGGCCCCACAGAGTGTATGACTG
TGGCTCTCACTCGCTCTCAGACTAAGACCCCAACCCAAATAGGGAGGGAGAGGGAAAGGCG
ATACATCCTCCCCACCGCAGGCACCCGGGGCTGGAGGGCGTGTACCAAATCCCGCG
CCATCAGCCTGGATGGCATAAGTAGATAAAACTGTGAGCTCGCACACCGAAAGGGCCT
GACCCCTACTTAGCTCCCTCTGAAACAAAGAGCAGACTGTGGAGAGCTGGAGAGCGCA
GCCAGCTCGCTTTGCTGAGAGCCCCCTTGACAGAAAGCCCAGCACGACCCCTGCTGGAAG
AACTGACAGTGCCCTGCCCTCGGCCCCGGGCCTGTGGGTTGGATGCCCGGTTCTATAC
ATATATACATATCCACATCTATATAGAGAGATAGATATCTATTTCCCTGTGGATTAG
CCCCGTGATGGCTCCCTGTTGGTACGCAGGGATGGCAGTTGCACGAAGGCATGAATGTAT
TGTAAATAAGTAACCTTGACTTCTGAC

FIGURE 34

MLLWILLLETSLCFAAGNVTGVCKEKICSCNEIEGDLHVDCEKKGFTSLQRFTAPTSQFYH
LFLHGNSLTRLFPNEFANFYNAVSLHMENNLHEIVPG AFLGLQLVKRLHINNNKIKSFRKQ
TFLGLDDLEYLQADFNLLRIDPGAFQDNLKLEVLIILNDNLISTLPANVFQYVPITHLDLRG
NRLKTL PYEEVLEQIPGIAEILLEDPWDCTCDLLSLKEWLENIPKNALIGRVVCEAPTRLQ
GKDLNETTEQDLCPLKNRVDSSLAPPQAQEETFAPGPLPTPKTNGQEDHATPGSAPNGGT
IPGNWQIKIRPTAAIATGSSRNKPLANSLPCPGCSDHIPGSGLKMNCNNRNVSSLADLK
KLSNVQELFLRDNIHSIRKSHFDYKNLILLLDGNNNIATVENNTFKNLLDLRWLYMDSNY
LDTLSREKFAGLQNLEYLNVEYNQIQLILPGTFNAMPKLRILILNNNLLRSLPVDFAGVSL
SKLSLHN NYFM YLPVAGVLDQLTSIIQIDLHGNPWECSCTIVPFKQWAERLGSEVLMSDLKC
ETPVNFFRKDFM LLSNDEICPQLYARISPTLTSHSKNSTGLAETGTHNSYLDTSRVSISVL
VPGLL VFVTS AFTVV GMLV F I LRNRKR SKRR DANSSA EINSI QTVC DSSYWHNG PYNADG
AHRVYDCGSHSLSD

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 618-638

N-glycosylation site.

amino acids 18-22, 253-257, 363-367, 416-420, 595-599, 655-659

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 122-126, 646-650

Casein kinase II phosphorylation site.

amino acids 30-34, 180-184, 222-226, 256-260, 366-370, 573-577,
608-612, 657-661, 666-670, 693-697

N-myristoylation site.

amino acids 17-23, 67-73, 100-106, 302-308, 328-334, 343-349,
354-360, 465-471, 493-499, 598-604, 603-609

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 337-348

FIGURE 35

AGTCGACTGCGTCCCCTGTACCCGGGCCAGCTGTGTTCTGACCCCAGAATAACTCAGGGC
TGCACCGGGCCTGGCAGCGCTCCGCACACATTCTCTGCGGGCTAAGGGAAACTGTTGGC
CGCTGGGCCCGGGGGGATTCTTGGCAGTTGGGGGTCGTCGGAGCGAGGGCGGAGGGG
AAGGGAGGGGGAACCGGGTTGGGAAGCCAGCTGTAGAGGGCGGTGACCGCGCTCAGACAC
AGCTCTGCGTCCTCGAGCGGACAGATCCAAGTTGGGAGCAGCTCTGCGTGCGGGCCTCAG
AGAATGAGGCCGGCTCGCCCTGTGCCTCCTCTGGCAGGCCTCTGGCCCGGGCCGGCGG
CGGCGAACACCCCCACTGCGGACCGTGTGGCTCGCTCGGCCCTGGGGCCTGCTACAGCCTGC
ACCACGCTACCATGAAGCGGCAGGGGCCGAGGGAGGCCTGCATCCTGCGAGGTGGGGCGCTC
AGCACCGTGCCTGCAGCTGCGCGCTGTGCTCGCGCTCCTGCGGGCAGGCCAGG
GCCCGGAGGGGGCTCAAAGACCTGCTGTTCTGGGTGCAGTGGAGCGCAGGCCTCCACT
GCACCCCTGGAGAACGAGCCTTGCAGGGTTCTCCTGGCTGTCTCCGACCCGGGTCTC
GAAAGCGACACGCTGCAGTGGGTGGAGGAGCCCCAACGCTCTGCACCGCGGGAGATGCC
GGTACTCCAGGCCACCGTGGGTGAGCCCGCAGGCTGGAAGGAGATGCCATGCCACCTGC
GCGCCAACGGCTACCTGTGCAAGTACCAAGTTGAGGTCTTGTGCTCTGCGCCGCCCCGGG
GCCGCCTCTAACTTGAGCTATCGCGCCCTTCCAGCTGCACAGCGCCGCTCTGGACTTCAG
TCCACCTGGGACCGAGGTGAGTGCCTCTGCCGGGACAGCTCCGATCTCAGTTACTTGCA
TCGCGGACGAAATCGCGCTCGCTGGACAAACTCTCGGGCGATGTGTTGTGCCCTGCC
GGGAGGTACCTCCGTGCTGGCAAATGCCAGAGCTCCCTAACTGCCCTAGACGACTGGGAGG
CTTGCCTGCGAATGTGCTACGGGCTCGAGCTGGGAAGGACGGCGCTTGTGACCA
GTGGGGAGGACAGCCGACCCCTGGGGGACCGGGTGCCACCCAGGCCGGCCGGCCACT
GCAACCAGCCCCGTGCCGCAGAGAACATGGCCAATCAGGGTCGACGAGAACGACTGGGAGAGAC
ACCACTGTCCTGAACAAGACAATTCACTGTAACATCTATTCTGAGATTCTCGATGGGAT
CACAGAGCACGATGCTACCCCTCAAATGTCCTCAAGCCGAGTCAAAGGCCACTATCACC
CCATCAGGGAGCGTGAATTCAAAGTTAATTCTACGACTTCCTGCCACTCCTCAGGCTT
CGACTCCTCCTCTGCCGTGGCTTCATATTGTGAGCACAGCAGTAGTAGTGTGATCT
TGACCATGACAGTACTGGGCTGTCAAGCTGCTTCACGAAAGCCCTCTCAGCCA
AGGAAGGAGTCTATGGGCCGCCGGCTGGAGAGTGAACCTGAGGCCGCTGCTTGGCTC
CAGTTCTGCACATTGACAAACATGGGTGAAAGTCGGGACTGTGATCTGCCGGACAGAG
CAGAGGGTGCCTTGCAGGGAGTCCCTCTGGCTCTAGTGAATGCATAGGAAACAGGGGA
CATGGGCACTCCTGTGAACAGTTTCACTTTGATGAAACGGGAACCAAGAGGAACATTAC
TTGTGTAAGTACAATTCTGCAGAAATCCCCCTCCTCTAAATTCCCTTACTCCACTGAG
GAGCTAAATCAGAACTGCACACTCCTCCCTGATGATAGAGGAAGTGAAGTGCCTTAGGA
TGGTGAATCTGGGGACCGGGTAGTGCCTGGGAGAGATATTCTTATGTTATTGGAGAA
TTTGGAGAAGTGAATTCAAGACATTGAAACAAATAGAACACAATATAATTAC
TTAAAAAATAATTCTACCAAAATGGAAAGGAAATGTTCTATGTTGTCAGGCTAGGAGTAT
ATTGGTTCGAAATCCCAGGGAAAAAATAAAAATTAAGGATTGTTGAT

FIGURE 36

MRPAFALCLLWQALWPGPGGGEHPTADRAGCSASGACYSLHHATMKRQAAEEACILRGGALS
TVRAGAELRAVLALLRAGPGPGGGSKDLLFWVALERRSHCTLENEPLRGFSWLSSDPGGLE
SDTLQWVEEPQRSCTARRCAVLQATGGVEPAGWKEMRCHLRANGYLCKYQFEVLCAPRPGA
ASNLSYRAPFQLHSAALDFSPPGTEVSALCRGQLPISVTCIADEIGARWDKLSGDVLCPCPG
RYLRAGKCAELPNCLDDLGFACECATGFELGKDGRSCVTSGEGQPTLGGTGVPTRRPPATA
TSPVPQRTWPIRVDEKLGETPLVPEQDNSVTSIPEIPRWGSQSTMSTLQMSLQAESKATITP
SGSVISKFNSTTSSATPQAFDSSSAVVFIFVSTAVVVLVILTMVGLVKLCFHESPSSQPR
KESMGPPGLESDEPAALGSSAHCTNNGVKVGCDLRDRAEGALLAESPLGSSDA

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 399-418

N-glycosylation site.

amino acids 189-193, 381-385

Glycosaminoglycan attachment site.

amino acids 289-293

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 98-102, 434-438

Casein kinase II phosphorylation site.

amino acids 275-279, 288-292, 342-346, 445-449

N-myristoylation site.

amino acids 30-36, 35-41, 58-64, 59-65, 121-127, 151-157,
185-191, 209-215, 267-273, 350-356, 374-380, 453-459, 463-469,
477-483

Aspartic acid and asparagine hydroxylation site.

amino acids 262-274

FIGURE 37

CGGACGCGTGGATTCA
CGTCAGTCAGACGGCACCATAATCGCTTAAAAGTGCCTCCGCCCTGCCGGCGTATC
CCCCGGCTACCTGGGCCCGCCCGCGGGGTGCGCGCGTGAGAGGGAGCGCGCAGCGA
GCGCCGGTGTGAGCCAGCGCTGCTGCCAGTGTGAGCGCGGTGTGAGCGCGTGGGTGCGGA
GGGGCGTGTGAGCGCCACTCTGCCTGCTGGCTGCCGCCACCCAGCTCTCGCG
CAGCAGTCCCCAGAGAGACCTGTTTACATGTGGTGCATTCTACTGGAGAGTCTGGATT
TATTGGCAGTGAAGGTTTCTGGAGTGTACCCCTCAAATAGCAAATGTACTGGAAAATCA
CAGTTCCCAGAAGAAAAGTAGTCGTTCTCAATTCCGATTCAAGACCTCGAGAGTGACAAC
CTGTGCCGCTATGACTTGTGGATGTGTACAATGCCATGCCATGCCAGCGCATTGCCG
CTTCTGTGGCATTCCGGCTGGAGCCCTTGTGTCCAGTGGCAACAAGATGATGGTCAGA
TGATTCTGATGCCAACACAGCTGGCAATGGCTCATGCCATGTTCTCGCTGCTGAACCA
AACGAAAGAGGGGATCAGTATTGTGGAGGACTCCTTGACAGACCTCCGGCTTTAAAAC
CCCCAACTGCCAGACCGGATTACCCCTGCAGGAGTCACTTGTGTGGCACATTGTAGCCC
CAAAGAATCAGCTTATAGAATTAAAGTTGAGAAGTTGATGTGGAGCGAGATAACTACTGC
CGATATGATTATGTGGCTGTGTTAATGGCGGGAAAGTCAACGATGCTAGAAGAATTGGAAA
GTATTGTGGTGATAGTCCACCTGCGCCAATTGTGTCTGAGAGAAATGAACCTTATTCA
TTTATCAGACTTAAGTTAACTGCAGATGGTTATTGGTCACTACATATTCA
AAACTGCCTACAACACTACAGAACAGCCTGTCACCACATTCCCTGTAACCACGGTTAAA
ACCCACCGTGGCCTTGTCAACAAAAGTAGACGGACGGGACTCTGGAGGGCAATTATT
GTTCAAGTGA
TTGATTAGCCGGCACTGTTATCACAACCATCA
CTCGCGATGGGAGTTG
CACGCCACAGTCTCGATCATCAACATCTACAAAGAGGGAAATTGGCATT
CAGCAGGCGGG
CAAGAACATGAGTGCCAGGCTGACTGTCGCTGCAAGCAGTGCCCTCTCCT
CAGAACAGGGTC
TAAATTACATTATTATGGCCAAGTAGGTGAAGATGGCGAGGGAAAATCATGCC
AAACAGC
TTTATCATGATGTTCAAGACCAAGAACATCAGAACGCT
CTGGATGCC
TTAAAAATAAGCAATG
TTAACAGTGA
ACTGTCCATTAAAGCTGTATTCTGCCATTGCC
TTGAAAGATCTATGTT
TCTCAGTAGAAAAAAACTTATAAAATTACATATTCTGAAAGAGGATTCCGAAAGATGG
GA
CTGGTTGACTCTCACATGATGGAGGTATGAGGCCTCCGAGATAGCTGAGGG
AAGTTCT
TGCCTGCTGTCAGAGGAGCAGCTATGATTGAAACCTGCCACTTAGTC
GGTGTAGGA
AGCTAAAAGTGTCAAGCGTTGACAGCTGGAAAGCGTTATT
TACATCTGTAAAAGGAT
ATTTAGAATTGAGTTGTGAAGATGTCAAAAAAAGATTTAGAAGTGC
AAATTATTTAGT
GTTATTGTT
CACCTCAAGC
TTGCC
CTGAGGTGTACA
ATCTTGCTTGC
GTTTTCTA
AATCAATGCTTA
ATAAAATT
TTAAAGGAAAAAA

FIGURE 38

MRGANAWAPLCLLLAAATQLSRQQSPERPVFTCGGILTGESGFIGSEGFPGVYPPNSKCTWK
ITVPEGKVVVLNFRFIDLESDNLCRYDFVDVYNGHANGQRIGRFCGTFRPGALVSSGNKMMV
QMISDANTAGNGFMAMFSAAEPNERGDQYCGGLLDRPSGSFKTPNWPDRDYPAGVTCVWHIV
APKNQLIELKFEKFDVERDNYCRYDYAVFNGGEVNDARRIGKYCGDSPAPIVSERNELLI
QFLSDLSLTADGFIGHYIFRPKKLPTTEQPVTTFPVTTGLKPTVALCQQKCRRTGTLEGN
YCSSDFVLAGTVITTITRD GSLHATVSIINIYKEGNLAIQQAGKNMSARLTVVCKQCPLLRR
GLNYIIMQVGEDGRGKIMPNSFIMMFKTKNQKLLDALKNKQC

Signal sequence:

amino acids 1-23

N-glycosylation site.

amino acids 355-359

Casein kinase II phosphorylation site.

amino acids 64-68, 142-146, 274-278

Tyrosine kinase phosphorylation site.

amino acids 199-208

N-myristoylation site.

amino acids 34-40, 35-41, 100-106, 113-119, 218-224, 289-295,
305-311, 309-315, 320-326, 330-336

Cell attachment sequence.

amino acids 149-152

FIGURE 39

CGGACGCGTGGCGGACGCGTGGCGGCCACGGCGCCCGGGCTGGGCAGTCGCTTCTT
CCTTCTCCGTGGCCTACGAGGGTCCCAGCCTGGTAAAGATGGCCCCATGGCCCCGAAGG
GCCTAGTCCCAGCTGTGCTCTGGGCCTCAGCCTCTCCTCAACCTCCCAGGACCTATCTGG
CTCCAGCCCTCTCCACCTCCCCAGTCTTCTCCCCGCCTCAGCCCCATCCGTGTACACCTG
CCGGGGACTGGTTGACAGCTTAACAAGGGCTGGAGAGAACCATCCGGACAACCTTGAG
GTGGAAACACTGCCTGGGAGGAAGAGAATTGTCAAATAACAAAGACAGTGAGACCCGCCTG
GTAGAGGTGCTGGAGGGTGTGCAGCAAGTCAGACTCGAGTGCCACCGCCTGCTGGAGCT
GAGTGAGGAGCTGGTGGAGAGCTGGTGGTTACAAGCAGCAGGAGGCCGGACCTCTTCC
AGTGGCTGTGCTCAGATTCCCTGAAGCTCTGCTGCCCGCAGGCACCTCGGGCCCTCCTGC
CTTCCCTGTCTGGGAAACAGAGAGGCCCTGCGGTGGCTACGGCAGTGTGAAGGAGAAGG
GACACGAGGGGGCAGCGGGCACTGTGACTGCCAAGCCGGCTACGGGGTGAGGCCTGTGGCC
AGTGTGGCCTGGCTACTTGAGGCAGAACGCAACGCCAGCCATCTGGTATGTTGGCTTGT
TTTGGCCCTGTGCCGATGCTCAGGACCTGAGGAATCAAACGTGTTGCAATGCAAGAAGGG
CTGGGCCCTGCATCACCTCAAGTGTGAGACATTGATGAGTGTGGCACAGAGGGAGCCAAC
GTGGAGCTGACCAATTCTGCGTGAACACTGAGGGCTCCTATGAGTGCCGAGACTGTGCCAAG
GCCTGCCTAGGCTGCATGGGGCAGGCCAGGTGCTGTAAGAAGTGTAGCCCTGGCTATCA
GCAGGTGGCTCCAAGTGTCTGATGTGGATGAGTGTGAGACAGAGGTGTCCGGGAGAGA
ACAAGCAGTGTGAAAACACCGAGGGCGTTATCGCTGCATCTGTGCCGAGGGCTACAAGCAG
ATGGAAGGCATCTGTGTGAAGGAGCAGATCCAGAGTCAGCAGGCTTCTCAGAGATGAC
AGAAGACGAGTTGGTGGTGCAGCAGATGTTCTTGGCATCATCATCTGTGCACTGGCCA
CGCTGGCTGCTAAGGGCAGTGGTGTACCCGCATCTCATTGGGCTGTGGCGGCCATG
ACTGGCTACTGGTGTCAAGAGCAGTGGCTGGAGGGCTTCAAGGGCAGATA
ATCGCGGCCACCACCTGTAGGACCTCTCCCACCCACGCTGCCCGAGAGCTTGGCTGCC
TCCTGCTGGACACTCAGGACAGCTGGTTATTTGAGAGTGGGTAAGCACCCTACCTG
CCTTACAGAGCAGCCAGGTACCCAGGCCGGCAGACAAGGCCCTGGGGTAAAAAGTAGC
CCTGAAGGTGGATACCATGAGCTTCACTGGCGGGACTGGCAGGCTTCACAATGTGTGA
ATTTCAAAAGTTTCTTAATGGTGGCTGCTAGAGCTTGGCCCTGCTTAGGATTAGGTG
GTCCTCACAGGGTGGGCCATCACAGCTCCCTGCCAGCTGCATGCCAGTTCTGT
TCTGTGTTCACACATCCCCACACCCATTGCCACTATTATTCATCTCAGGAAATAAAGA
AAGGTCTGGAAAGTTAAAAAAAAAAAAAAAAAAAAAA

FIGURE 40

MAPWPKGLVPAVLWGLSLFLNLPPIWLQPSPPPQSSPPPQPHPCHTCRGLVDSFNKGLER
TIRDNFGGGNTAWEENLSKYKDSETRLVEVLEGVCSDKSFECRRLLELSEELVESWWFHKQ
QEAPDLFQWLCSDSLKLCGPAGTFGPSCLPCCPGTERPCGGYGCCEGEGTRGGSGHCDCQAG
YGGEACGQCGLGYFEAERNASHLVCSACFGPCARCSGPEESNLQCKKGWALHHLKCVDIDE
CGTEGANCGADQFCVNTEGSYECRDCAKACLGCMAGPGRCKCSPGYQQVGSKCLDVDECE
TEVCPGENKCENTEGGYRCICAEGYKQMEGICVKEQIPESAGFFSEMTEDELVVLQQMFFG
IIICALATLAAGDLVFTAIFIGAVAAMTGYWLSERSDRVLEGFIKGR

Signal sequence:

amino acids 1-29

Transmembrane domain:

amino acids 372-395

N-glycosylation site.

amino acids 79-83, 205-209

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 290-294

Casein kinase II phosphorylation site.

amino acids 63-67, 73-77, 99-103, 101-105, 222-226, 359-263

N-myristoylation site.

amino acids 8-14, 51-57, 59-65, 69-75, 70-76, 167-173, 173-179,
177-183, 188-194, 250-256, 253-259, 267-273, 280-286, 283-289,
326-332, 372-378, 395-401

Aspartic acid and asparagine hydroxylation site.

amino acids 321-333

EGF-like domain cysteine pattern signature.

amino acids 181-193

FIGURE 41

TGAGACCCTCCTGCAGCCTCTCAAGGGACAGCCCCACTCTGCCTCTTGCTCCTCCAGGGCA
GCACCATGCAGCCCCGTGGCTCTGCTGGCACTCTGGGTGTTGCCCTGGCCAGCCCCGGG
GCCGCCCTGACCGGGGAGCAGCTCCTGGCAGCCTGCTGCCAGCTGCAGCTAAAGAGGT
GCCCACCCCTGGACAGGGCCGACATGGAGGAGCTGGTCATCCCCACCCACGTGAGGGCCCAGT
ACGTGGCCCTGCTGCAGCGCAGCCACGGGGACCGCTCCCGCGAAAGAGGTTCAGCCAGAGC
TTCCGAGAGGTGGCCGGCAGGTTCTGGCGTTGGAGGCCAGCACACACCTGCTGGTGTTCGG
CATGGAGCAGCGGCTGCCGCCAACAGCGAGCTGGTCAGGCCGTGCTGCCGTCTTCAGG
AGCCGGTCCCCAAGGCCGCGTGCACAGGCACGGCGGCTGTCCCCGCGCAGCGCCGGGCC
CGGGTGACCGTCGAGTGGCTGCGCGTCCCGACGACGGCTCCAACCGCACCTCCCTCATCGA
CTCCAGGCTGGTGTCCGTCCACGAGAGCGGCTGGAAGGCCTTCGACGTGACCGAGGCCGTGA
ACTTCTGGCAGCAGCTGAGCCGGCCCGGCAGCCGCTGCTGCTACAGGTGTCGGTGCAGAGG
GAGCATCTGGGCCCGCTGGCGTCCGGCGCCACAAGCTGGTCCGCTTGCGCTCGCAGGGGGC
GCCAGCCGGCTGGGGAGCCCCAGCTGGAGCTGCACACCCCTGGACCTGGGGACTATGGAG
CTCAGGGCGACTGTGACCCCTGAAGCACCAATGACCGAGGGCACCGCTGCTGCCGCCAGGAG
ATGTACATTGACCTGCAGGGATGAAGTGGGCCAGAACTGGGTGCTGGAGCCCCGGCTT
CCTGGCTTATGAGTGTGTGGCACCTGCCGGCAGCCCCGGAGGCCCTGGCCTTCAAGTGGC
CGTTCTGGGCCCTGACAGTGCATGCCCTGGAGACTGACTCGCTGCCATGATGTCAGC
ATCAAGGAGGGAGGCAGGACCAGGCCAGGTGGTCAGCCTGCCAACATGAGGGTGCAGAA
GTGCAGCTGTGCCTCGGATGGTGCCTCGTGCCTGGAGGCTCCAGCCATAGGCGCCTAGTG
TAGCCATCGAGGGACTTGACTTGTGTGTTCTGAAGTGGTCCAGGGTACCAAGGAGAGCTG
GCGATGACTGAAGTGCATGGACAAATGCTCTGTGCTCTAGTGAGCCCTGAATTGCTT
CCTCTGACAAGTTACCTCACCTAATTTGCTCTCAGGAATGAGAATCTTGGCCACTGGA
GAGCCCTGCTCAGTTCTCTATTCTTACTGCACATATTCTAACGACTTACAT
GTGGAGATACTGTAACCTGAGGGCAGAAAGCCANTGTGTCATTGTTACTGTCTGTAC
TGGATCTGGCTAAAGTCCTCCACCACCTCTGGACCTAACGACCTGGGTTAAGTGTGGGT
TGTGCATCCCCAATCCAGATAATAAGACTTTGTAAAACATGAATAAACACATTATTCT
AAAAA

FIGURE 42

MQPLWLCWALWVLPLASPGAAALTGEQLLGSLLRQLQLKEVPTLDRADMEELVIPTHVRAQYV
ALLQRSHGDRSRGKRFQSFRREVAGRFLALEASTHLLVFGMEQLLPPNSELVQAVLRLFQEP
VPKAALHRHGRLSPRSARARVTVEWLVRDDGSNRTSLIDSRLVS VHESGWKAFDVTEAVNF
WQQLSRPRQPLLQSVQREHLGPLASGAHKLVRFASQGAPAGLGEPQLELHTLDLGDYGAQ
GDCDPEAPMTEGTRCCRQEMYIDLQGMKWAENWVLEPPGFLAYECVGTCRQPPEALAFKWPF
LGPRQCIASETDSLPMIVSIKEGGRTQPQVSLPNMRVQKCSCASDGALVPRRLQP

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 158-162

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 76-80

Casein kinase II phosphorylation site.

amino acids 68-72, 81-85, 161-165, 169-173, 319-323, 329-333

N-myristoylation site.

amino acids 19-25, 156-162, 225-231, 260-266, 274-280

Amidation site.

amino acids 74-78

TGF-beta family signature.

amino acids 282-298

069001532 - 024201

FIGURE 43

GTCTGTCAGGGAGTCCCTCGCGCTGTTGTCAGTGGCCTGATCGC**GATGGGACAAA**
GGCGCAAGTCGAGAGGAAACTGTTGTCCTCTCATATTGGCGATCCTGTTGCTCCCTGG
CATTGGGCAGTGTACAGTGCACTCTTCTGAACCTGAAGTCAGAATTCCCTGAGAATAATCCT
GTGAAGTTGTCCTGTGCCTACTCGGGCTTTCTTCTCCCCGTGGAGTGGAGTTGACCA
AGGAGACACCACCAAGACTCGTTGCTATAATAACAAGATCACAGCTCCTATGAGGACCGGG
TGACCTTCTTGCCA**ACTGGTATCACCTCAAGTCCGTGACACGGGAAGACACTGGGACATAC**
ACTTGTATGGTCTCTGAGGAAGGCGGAAACAGCTATGGGGAGGTCAAGGTCAAGCTCATCGT
GCTTGTGCCTCCATCCAAGCCTACAGTTAACATCCCCTCCTGCCACCATTGGAACCGGG
CAGTGCTGACATGCTCAGAACAAAGATGGTCCCCACCTTCTGAATAACACCTGGTCAAAGAT
GGGATAGTGTGCTACGAATCCAAAAGCACCCGTGCCTCAGCAACTCTCCTATGTCCT
GAATCCCACAAACAGGAGAGCTGGTCTTGATCCCCTGTCAGCCTCTGATACTGGAGAATACA
GCTGTGAGGCACGGAATGGTATGGACACCCATGACTTCAAATGCTGTGCGCATGGAAGCT
GTGGAGCGGAATGTGGGGTCATCGTGGCAGCCGTCTGTAACCTGATTCTCTGGGAAT
CTTGGTTTTGGCATCTGGTTGCCTATAGCCGAGGCCACTTGACAGAACAAAGAAAGGGA
CTTCGAGTAAGAAGGTGATTACAGCCAGCCTAGTGCCGAAGTGAAGGAGAATTCAAACAG
ACCTCGTCATTCTGGTGT**GAGCCTGGCTCGCCTACCGCCTATCATCTGCATTGCCCTACT**
CAGGTGCTACCGGACTCTGGCCCTGATGTCGTAGTTCACAGGATGCCCTATTGCTTC
TACACCCCACAGGGCCCCCTACTTCTGGATGTGTTTAATAATGTCAGCTATGTGCC
ATCCTCTTCATGCCCTCCCTCCCTTACCACTGCTGAGTGGCCTGGAACTGTTAAA
GTGTTATTCCCCATTCTTGAGGGATCAGGAAGGAATCCTGGGTATGCCATTGACTTCCC
TTCTAAGTAGACAGCAAAATGGCGGGGTCGCAGGAATCTGCACTCAACTGCCACCTGGC
TGGCAGGGATCTTGAATAGGTATCTTGAGCTTGGTCTGGCTCTTCCCTGTACTGAC
GACCAGGGCCAGCTGTTCTAGAGCGGAATTAGAGGCTAGAGCGGCTGAAATGGTTGG
TGATGACACTGGGTCCCTCATCTGGGCCACTCTCTGTCCTGCTTCCATGGGAAGTG
CCACTGGATCCCTCTGCCCTGTCCTCTGAATACAAGCTGACTGACATTGACTGTCTGT
GGAAAATGGGAGCTTGTGGAGAGCATAGTAAATTTCAGAGAACCTGAAGCCAAAAG
GATTTAAAACCGCTGCTCTAAAGAAAAGAAAACTGGAGGCTGGCGCAGTGGCTCACGCC
TAATCCCAGAGGCTGAGGCAGGCGGATCACCTGAGGTGGAGTCAGGATCAGCCTGACCA
ACATGGAGAAACCCACTGGAAATACAAAGTTAGCCAGGCATGGTGGTGCATGCCCTGAGTC
CCAGCTGCTCAGGAGCCTGGCAACAAAGAGCAAAACTCCAGCTCAAAAAAAAAAAAAAA

FIGURE 44

MGTKAQVERKLLCLFILAILLCSLALGSVTVHSSEPEVRIPENNPKLSCAYSGFSSPRVEW
KFDQGDTTRLCYNNKITASYEDRVTFLPTGITFKSVTREDTGTYTCMVSEEGGNSYGEVKV
KLIVLVPPSKPTVNIPSSATIGNRAVLTSEQDGSPPEYTWFKDGIQMPTNPKSTRAFSNS
SYVLNPTTGELVFDPLSASDTGEYSCEARNGYGTPMTSNAVRMEAVERNVGVIVAAVLVTLI
LLGILVFGIWFAYSRGHFDRTKKGTSSKKVIYSQPSARSEGEGFKQTSSFLV

Signal sequence:

amino acids 1-27

Transmembrane domain:

amino acids 238-255

N-glycosylation site.

amino acids 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 270-274

Casein kinase II phosphorylation site.

amino acids 34-38, 82-86, 100-104, 118-122, 152-156, 154-158,
193-197, 203-207, 287-291

N-myristoylation site.

amino acids 105-111, 116-122, 158-164, 219-225, 237-243, 256-262

FIGURE 45

CAGCGCGTGGCCGGCGCCGTGTGGGACAGC**ATGAGCGCGGTTGGATGGCGCAGGTTGGA**
GCGTGGCGAACAGGGCTCTGGCCTGGCGCTGCTGCTGCTCGGCCTCGGACTAGGCCT
GGAGGCCGCGCGAGCCCCTTCCACCCGACCTCTGCCAGGCCAGGCCAGCTCAG
GCTCGTGCCACCCACCAAGTTCCAGTGCCGCACCAGTGGCTATGCGTGCCCTCACCTGG
CGCTGCGACAGGGACTTGGACTGCAGCGATGGCAGCGATGAGGAGGAGTGCAGGATTGAGCC
ATGTACCCAGAAAGGGCAATGCCAACCGCCCCCTGGCCTCCCTGCCCTGCACCGCGTCA
GTGACTGCTCTGGGGAACTGACAAGAAACTGCGCAACTGCAGCCGCTGGCCTGCCTAGCA
GGCGAGCTCCGTTGCACGCTGAGCGATGACTGCATTCCACTCACGTGGCGCTGCGACGGCCA
CCCAGACTGTCCCGACTCCAGCGACGAGCTGGCTGTGGAACCAATGAGATCCTCCGGAAG
GGGATGCCACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTACCTCTCAGGAATGCC
ACAACCATGGGGCCCCCTGTGACCCCTGGAGAGTGTCCCTCTGTCGGAATGCCACATCCTC
CTCTGCCGGAGACCAGTCTGGAAGCCCAACTGCCCTATGGGTTATTGAGCTGCTGCGGTGC
TCAGTGCAAGCCTGGTCACCGCCACCCCTCCTCTTGTCCCTGGCTCCGAGCCCAGGAGCGC
CTCCGCCACTGGGTTACTGGTGGCCATGAAGGAGTCCCTGCTGTCAGAACAGAAGAC
CTCGCTGCC**TGAGGACAAGCAACTTGCACCCACCGTCACTCAGCCCTGGCGTAGCCGGACA**
GGAGGAGAGCAGTGATGCGGATGGGTACCCGGCACACCAGCCCTCAGAGACCTGAGTTCTT
CTGGCCACGTGGAACCTCGAACCCGAGCTCCTGCAGAAGTGGCCCTGGAGATTGAGGGTCCC
TGGACACTCCCTATGGAGATCCGGGGAGCTAGGATGGGAACCTGCCACAGCCAGAACTGAG
GGGCTGGCCCCAGGCAGCTCCAGGGGTAGAACGCCCTGTGCTTAAGACACTCCCTGCTG
CCCCGTCTGAGGGTGGCGATTAAAGTTGCTTC

FIGURE 46

MSGGWMAQVGAWRTGALGLALLLLGLGLGLEAAASPLSTPTSAQAAGPSSGSCPPTKFQCR
TSGLCVPLTWRCDRDLDSDGSDEEECRIEPCTQKGQC PPPGLPCPCTGVSDCSGGTDKKL
RNCSRRLACLAGELRCTLSDDCIPLTWRCDGHPDCPDSSDELCGGTNEILPEGDATTMGPPVT
LESVTSLRNATTMGPVTLESVPSVGNATSSSAGDQSGSPTAYGVIAAAAVLSASLVTATLL
LLSWLRAQERLRPLGLLVAMKESLLLSEQKTSLP

Signal sequence:

amino acids 1-30

Transmembrane domain:

amino acids 230-246

N-glycosylation site.

amino acids 126-130, 195-199, 213-217

Casein kinase II phosphorylation site.

amino acids 84-88, 140-144, 161-165, 218-222

N-myristoylation site.

amino acids 3-9, 10-16, 26-32, 30-36, 112-118, 166-172, 212-218,
224-230, 230-236, 263-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 44-55

Leucine zipper pattern.

amino acids 17-39

FIGURE 47

898

CCCCACCGCGTCCGGTCTCGCTCGCTCGCGCAGCAGCGGGCAGCAGAGGTGCGCACAGATGCGG
GTTAGACTGGCGGGGGAGGAGGCGGAGGAAGGAAGGAAAGCTGCATGCATGAGACCCACAGA
CTCTTGCAAGCTGGATGCCCTCTGTGGATGAAAGATGTTATCATGGAATGAACCCGAGCAATG
GAGATGGATTCTAGAGCAGCAGCAGCAGCAGCAACCTCAGTCCCCCAGAGACTCTTG
GCCGTGATCCTGTGGTTCAGCTGGCGCTGTGCTCGGCCCTGCACAGCTCACGGCGGGTT
CGATGACCTTCAAGTGTGTGCTGACCCGGCATTCCGAGAATGGCTTCAGGACCCCCAGCG
GAGGGGTTTCTTGAGGCTCTGTAGCCGATTTCACTGCCAAGACGGATTCAAGCTGAAG
GGCGCTACAAAGAGACTGTGTTGAAGCATTAAATGGAACCTAGGCTGGATCCAAGTGA
TAATTCCATCTGTGTGCAAGAAGATTGCCGTATCCCTCAAATCGAAGATGCTGAGATTATA
ACAAGACATATAGACATGGAGAGAAGCTAACATCACTTGTATGAAGGATTCAAGATCCGG
TACCCCGACCTACACAATATGGTTTCAATTGTGCGATGATGGAACGTGGAATAATCTGCC
CATCTGTCAAGGCTGCCTGAGACCTCTAGCCTCTTAATGGCTATGTAACATCTGAGC
TCCAGACCTCCTCCGGTGGGACTGTGATCTCCTATCGCTGCTTCCGGATTAAACTT
GATGGGTCTGCGTATCTTGAGTGCTTACAAAACCTTATCTGGTCGTCCAGCCCACCCGGTG
CCTTGCTCTGGAAGCCAAGTCTGTCCACTACCTCCAATGGTGAGTCACGGAGATTCTGTCT
GCCACCCGGCCCTGTGAGCGCTACAAACCACGGAACGTGTTGGAGTTACTGCGATCCT
GGCTACAGCCTCACCAAGCGACTACAAGTACATCACCTGCCAGTATGGAGAGTGTTCCCTTC
TTATCAAGTCTACTGCATCAAATCAGAGCAAACGTGGCCAGCACCCATGAGACCCCTCTGA
CCACGTGGAAGATTGTGGCGTTCACGGCAACCAGTGTGCTGCTGGTGTGCTCGTCATC
CTGGCCAGGATGTTCCAGACCAAGTTCAAGGCCACTTCCCCCAGGGGCCTCCCGGAG
TTCCAGCAGTGACCCCTGACTTGTGGTAGACGGCGTCCGTATGCTCCGTCTATG
ACGAAGCTGTGAGTGGCGCTTGAGTGCTTAGGCCCGGGTACATGGCCTCTGTGGCCAG
GGCTGCCCTTACCGTGGACGACCAGAGCCCCCAGCATACCCGGCTCAGGGACACGGA
CACAGGCCAGGGAGTCAGAAACCTGTGACAGCGTCTCAGGCTTTCTGAGCTGCTCCAAA
GTCTGTATTCACCTCCAGGTGCCAAGAGAGCACCACCCAGCTGCTCGGACAACCTGACATA
ATTGCCAGCACGGCAGAGGGAGGTGGCATCCACCAGCCCAGGCATCCATCATGCCACTGGGT
GTTGTTCTAAGAAACTGATTGATTAAAAAATTCCAAAGTGTCTGAAGTGTCTTTCAA
ATACATGTTGATCTGTGGAGTTGATTCCCTTCTCTTGGTTAGACAAATGTAACAA
AGCTCTGATCCTTAAAATTGCTATGCTGATAGAGTGAGGGCTGGAAGCTGATCAAGTC
CTGTTCTTCTTGACACAGACTGATTTAAAAGNAAAAAA

FIGURE 48

MYHGMNPSNGDGFLEQQQQQQPQSPQRLLAVILWFQLALCFGPAQLTGGFDDLQVCADPGI
PENGFRTPSGGVFFEGSVARFHCQDGFKLKAGTKRLCLKHFNGTLGWIPSDNSICVQEDCRI
PQIEDAEIHNKTYRHGEKLIITCHEGFKIRYPDLHNMVSLCRDDGTWNNLPICQGCLRPLAS
SNGYVNISELQTSFPVGTVISYRCFPGFKLDGSAYLECLQNLIWSSSPRCLALEAQVCPLP
PMVSHGDFVCHPRPCERYNHGTVVEFYCDPGYSLTSDYKYITCQYGEWFPSYQVYCIKSEQT
WPSTHETLLTTWKIVAFATSVLLVLLVILARMFQTKFKAHFPPRGPPRSSSDPDFVVVD
GVPVMLPSYDEAVSGGLSALGPGYMASVGQGCPLPVDDQSPPAYPGSGDTDTGPGESETCDS
VSGSSELLQSLYSPPRCQESTHPASDNPDIIASTAEVASTSPGIHHAHWVLFLRN

Signal sequence:

amino acids 1-41

Transmembrane domain:

amino acids 325-344

N-glycosylation site.

amino acids 104-108, 134-138, 192-196

Casein kinase II phosphorylation site.

amino acids 8-12, 146-150, 252-256, 270-274, 313-317, 362-366,
364-368, 380-384, 467-471, 468-472

N-myristoylation site.

amino acids 4-10, 61-67, 169-175, 203-209, 387-393, 418-424,
478-484

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 394-405

FIGURE 49

CCCACGCGTCCGCTCCGCCCTCCCCCGCCTCCCGTGCAGTCGGTCCGGTGGCCTAGAGA
TGCTGCTGCCCGGGTTGCAGTTGTGCAGCAGCCTCTGCCGCCAGCCGCTCCACCGCCGT
AGCGCCCGAGTGTCCGGGGGGCGCACCCGAGTCGGGCCATGAGGCCGGAACCGCGCTACAGG
CCGTGCTGCCGGTGCCTGGTGGGCTGCCGCCGACGGGTCGCCGTGAGTGCCT
TCGGATTGGACCTCAGAGGAGGGCAGCCAGTCTGCCGGGAGGGACACAGAGGCCTTGTAA
TAAAGTCATTACTTCATGATACTTCTGAAGACTGAACCTTGAGGAAGCCAAGAACGCT
GCAGGAGGGATGGAGGCCAGCTAGTCAGCATCGAGTCTGAAGATGAACAGAAACTGATAGAA
AAGTTCATGAAAACCTCTGCCATCTGATGGTACTTCTGGATTGGCTCAGGAGGCCTGA
GGAGAAACAAAGCAATAGCACAGCCTGCCAGGACCTTATGCTTGGACTGATGGCAGCATAT
CACAAATTAGGAACCTGGTATGTGGATGAGCCGTCCTGCCAGGAGGTCTGCCGTGGTCATG
TACCATCAGCCATCGGCACCCGCTGGCATCGGAGGCCCTACATGTTCCAGTGGAAATGATGA
CCGGTGCAACATGAAGAACATTCATTGCAAATATTCTGATGAGAACACCAGCAGTCCT
CTAGAGAAGCTGAAGGTGAGGAAACAGAGCTGACAACACCTGTACTTCCAGAAGAACACAG
GAAGAAGATGCCAAAAAACATTAAAGAAAGTAGAGAACGCTGCCCTGAATCTGCCCTACAT
CCTAATCCCCAGCATTCCCTCTCCTCCTGTGGTCACCACAGTTGTATGTTGGTT
GGATCTGTAGAAAAAGAAAACGGGAGCAGCCAGACCTAGCACAAAGAACACACCAC
TGGCCCTCTCCTCACCAAGGAAACAGCCGGACCTAGAGGTCTACAATGTCATAAGAAAACA
AAGCGAAGCTGACTTAGCTGAGACCCGGCCAGACCTGAAGAATATTCTATTCCAGTGTGTT
CGGGAGAAGCCACTCCGATGACATGTCTTGTACTATGACAACATGGCTGTGAACCCATCA
GAAAGTGGTTGTGACTCTGGTGGAGAGTGGATTGTGACCAATGACATTATGA
GTTCTCCCCAGACAAATGGGAGGAGTAAGGAGTCTGGATGGTGGAAAATGAAATATATG
GTTATTAGGACATATAAAAACTGAAACTGACAACAAATGGAAAAGAAATGATAAGCAAAATC
CTCTTATTTCTATAAGAAAATACACAGAAGGTCTATGAACAAGCTTAGATCAGGTCTGT
GGATGAGCATGTGGTCCCCACGACCTCTGGACCCACGTTGGCTGTATCCTTAT
CCCAGCCAGTCATCCAGCTGACCTTATGAGAAGGTACCTGCCAGGTCTGGCACATAGTA
GAGTCTCAATAATGTCATTGGTTGGTTGTATCTAACCTTAAGGGACAGAGCTTACCTG
GCAGTGATAAAAGATGGGCTGTGGAGCTGGAAAACCACCTCTGTTTCTGCTATACAG
CAGCACATATTATCATACAGACAGAAAATCCAGAATCTTCAAAGCCCACATATGGTAGCACAG
GTTGGCCTGTGCATGGCAATTCTCATATCTGTTTTCAAAGAATAAAATCAAATAAAGA
GCAGGAAAAAA

FOOTNOTE 660

FIGURE 50

MRPGTALQAVLLAVLLVGLRAATGRLLSASDLRGGQPVCRRGTQRPCYKVIYFHDTSRRL
NFEEAKEACRRDGGQLVSIESEDEQKLIENLLPSDGDFWIGLRRREEKQSNSTACQDL
YAWTDGSISQFRNWYVDEPSCGSEVCVVMYHQPSAPAGIGGPYMFQWNDDRCNMKNFICKY
SDEKPAVPSREAEGEETELTPVLPEETQEEDAKTFKESREAALNAYILIPSIPLLLL
VTTVVCWVWICRKRKREQPDPTKKQHTIWPSPHQGNSPDLEVYNVIRKQSEADLAETRPDL
KNISFRVCSGEATPDDMSCDYDNMAVNPSSEGFTLVSVESGFVTNDIYEFS PDQMGRSKES
GWVENEIYGY

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 117-121, 312-316

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 296-300

Casein kinase II phosphorylation site.

amino acids 28-32, 30-34, 83-87, 100-104, 214-218, 222-226,
299-303, 306-310, 323-327

N-myristoylation site.

amino acids 18-24, 37-43, 76-82, 146-152

FIGURE 51

GGGGTCTCCCTCAGGGCCGGGAGGCACAGCGGTCCCTGCTGAAGGGCTGGATGTACGC
ATCCGCAGGTTCCCGCGGACTTGGGGCGCCCGCTGAGCCCCGGCGCCCGAGAAGACTTGT
GTTGCCTCCTGCAGCCTCAACCCGGAGGGCAGCGAGGGCCTACCACCATGATCACTGGTGT
GTTCAGCATGCGCTTGTGGACCCCAGTGGCGTCCTGACCTCGCTGGCGTACTGCCTGCACC
AGCGGCGGGTGGCCCTGGCCGAGCTGCAGGAGGCCATGGCCAGTGTCCGGTCGACCGCAGC
CTGCTGAAGTTGAAAATGGTGCAGGTGCGTTTGACACACGGGCTGGAGTCCTCTCAAGCC
GCTCCGCTGGAGGAGCAGGTAGAGTGGAACCCCCAGCTATTAGAGGTCCCACCCAAACTC
AGTTGATTACACAGTCACCAATCTAGCTGGTGGTCCGAAACCATATTCTCCTTACGACTCT
CAATACCATGAGACCACCCCTGAAGGGGGCATGTTGCTGGCAGCTGACCAAGGTGGCAT
GCAGCAAATGTTGCCTTGGGAGAGAGACTGAGGAAGAACTATGTGGAAGACATTCCCTTC
TTTCACCAACCTTCAACCCACAGGAGGTCTTATTGTTCCACTAACATTTCGGAATCTG
GAGTCCACCCGTTGTTGCTGGCTGGCTTTCCAGTGTCAAGAAAGAAGGACCCATCATCAT
CCACACTGATGAAGCAGATTAGAAGTCTTGTATCCAACTACCAAAGCTGCTGGAGCCTGA
GGCAGAGAACCAAGAGGCCGGAGGCAGACTGCCTCTTACAGCCAGGAATCTCAGAGGATTG
AAAAAGGTGAAGGACAGGATGGCATTGACAGTAGTGTGATAAAAGTGGACTCTTCATCCTCCT
GGACAACGTGGCTGCCAGCAGGCACACAACCTCCAAGCTGCCCATGCTGAAGAGATTG
CACGGATGATCGAACAGAGAGACTGTGGACACATCCTGTACATACTGCCAAGGAAGACAGG
GAAAGTCTTCAGATGGCAGTAGGCCATTCCACATCCTAGAGAGCAACCTGCTGAAAGC
CATGGACTCTGCCACTGCCCGACAAGATCAGAAAGCTGTATCTATGCGGCTCATGATG
TGACCTTCATACCGCTTTAATGACCCCTGGGATTTTGACCACAAATGCCACCGTTGCT
GTTGACCTGACCATGGAACCTTACAGCACCTGGAATCTAAGGAGTGGTTGTGCAGCTCTA
TTACCACGGGAAGGAGCAGGTGCCAGAGGTTGCCCTGATGGGCTCTGCCGCTGGACATGT
TCTTGAATGCCATGTCAGTTATACCTTAAGCCCAGAAAAATACCATGCACTCTGCTCTCAA
ACTCAGGTGATGGAAGTTGGAAATGAAGAGTAACTGATTATAAAAGCAGGATGTGTTGATT
TTAAAATAAGTGCCTTATACAATG

FIGURE 52

MITGVFSMRLWTPGVVLTSAYCLHQRRVALAELQEADGQCPVDRSLLKLKMVQVVFRHGAR
SPLKPLPLEEQVEWNPQLLEVPPQTQFDYTVTNLAGGPKPYSPYDSQYHETTLKGGMFAGQL
TKVGMQQMFALGERLRKNYVEDIPFLSPTFNQEVFIRSTNIFRNLESTRCLLAGLFQCQKE
GPIIIHTDEADSEVLYPNYQSCWSLRQRTRGRQTASLQPGISEDLKKVKDRMGIDSSDKVD
FFILLDNVAEQAHLNPSCPMLKRFARMIEQRAVDTSLYILPKEDRESLQMAVGPFHLILES
NLLKAMDSATAPDKIRKLYLYAAHDVTFIPLLMTLGIFDHKWPPFAVDLTMELYQHLESKEW
FVQLYYHGKEQVPRGCPDGLCPLDMFLNAMSVTLSPEKYHALCSQTQVMVEVGNEE

Signal sequence:

amino acids 1-23

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 218-222

Casein kinase II phosphorylation site.

amino acids 87-91, 104-108, 320-324

Tyrosine kinase phosphorylation site.

amino acids 280-288

N-myristoylation site.

amino acids 15-21, 117-123, 118-124, 179-185, 240-246, 387-393

Amidation site.

amino acids 216-220

Leucine zipper pattern.

amino acids 10-32

Histidine acid phosphatases phosphohistidine signature.

amino acids 50-65

FIGURE 53

CTCCTCTAACATACTTGCAGCTAAACTAAATATTGCTGCTGGGACCTCCTCTAGCCT
TAAATTCAGCTCATCACCTCACCTGCCTGGTCATGGCTCTGCTATTCTCCTTGATCCTT
GCCATTTGCACCAGACCTGGATTCCCTAGCGTCTCCATCTGGAGTGC~~GG~~CTGGTGGGGGGCCT
CCACCGCTGTGAAGGGCGGGTGGAGGTGGAACAGAAAGGCCAGTGGGCACC~~GT~~GATG
ACGGCTGGGACATTAAGGACGTGGCTGTGTTGCCGGAGCTGGCTGTGGAGCTGCCAGC
GGAACCCCTAGTGGTATTTGTATGAGCCACCAGCAGAAAAAGAGCAAAGGT~~CCT~~CATCCA
ATCAGTCAGTTGCACAGGAACAGAAGATA~~C~~ATTGGCTCAGTGTGAGCAAGAAGAAGTTATG
ATTGTTCACATGATGAAGATGCTGGGCATCGTGTGAGAACCCAGAGAGCTTTCTCCCCA
GTCCCAGAGGGTGT~~C~~AGGCTGGCTGACGGCC~~T~~GGCATTGCAAGGGAC~~G~~CGT~~G~~GAAGTGA
GCACCAGAACCA~~G~~GTGGTACCGTGTGCCAGACAGGCTGGAGC~~T~~CCGGCCGAAAGGTGG
TGTGCCGGCAGCTGGGATGTGGGAGGGCTGTACTGACTCAAAACGCTGCAACAAGCATGCC
TATGGCCGAAAACCCATCTGGCTGAGCCAGATGTCATGCTCAGGACGAGAAGCAACCC~~T~~CA
GGATTGCC~~T~~CTGGC~~T~~GGGGAAAGAACACCTGCAACC~~A~~ATGATGAAGACACGTGGTCG
AATGTGAAGATCC~~T~~TGACTTGAGACTAGTAGGAGGAGAACACCTCTGCTCTGGCGACTG
GAGGTGCTGCACAAGGGCGTATGGGCTCTGTC~~T~~GTGATGACA~~A~~CTGGGAGAAAGGAGGA
CCAGGTGGTATGCAAGCAACTGGGCTGTGGAA~~G~~TCCCTCTCC~~C~~CTCAGAGACCGGA
AATGCTATGCC~~T~~GGGGTTGCCGCATCTGGCTGGATAATGTTGCTCAGGGAGGAG
CAGTCC~~C~~GGAGCAGTGC~~C~~CAGCACAGATTTGGGGTT~~C~~ACGACTGCACCCACCAGGAAGA
TGTGGCTGTCATCTGCTCAGTGTAGGTGGC~~A~~T~~C~~ATCTAATCTGTTGAGTGC~~C~~TAATAGAA
GAAAAACACAGAACAGAACAGGAGCATTACTGTC~~A~~ACTGCATGGGATGAACACTGATCT
TCTTCTGCC~~T~~GGACTGGACTTATACTTGGT~~G~~CCCTGATTCTCAGGCC~~T~~TCAGAGTTGG
ATCAGAACTTACAACATCAGGTCTAGTTCTCAGGCC~~A~~T~~C~~AGACATAGTTGGA~~A~~CTACATCA
CCACCTTC~~C~~TATGTC~~C~~CACATTGCACACAGCAGATTCCAGC~~T~~CCATAATTGTGT~~T~~
CAACTACTAAATACATTCTCACACACACACACACACACACACACACACACACATA
CACCA~~T~~TGTC~~T~~GT~~T~~GAAGAA~~C~~CTGACAAAATACAGATTTGGTACTGAAAGAGA
TTCTAGAGGAAC~~G~~GAATT~~T~~TAAGGATAAATT~~T~~CTGAATTGGTTATGGGTTCTGAAATTG
GCTCTATAATCTAATTAGATATAAAATTCTGGTAAC~~T~~TATTACAATAAAAGATAGCAC
TATGTGTTCAA

FIGURE 54

MALLFSLILAICTRPGFLASPSGVRLVGLHRCEGRVEVEQKGQWGTVCDDGWDIKDVAVL
RELGCGAASGTPSGILYEPPAEKEQKVLIQSVSCTGTEDTLAQCEQEEVYDCSHDEDAGASC
ENPESSFSPVPEGVRLADGPGHCKGRVEVKHQNQWYTVCQTGWSLRAAKVVCRQLGCGRAVL
TQKRCNKHAYGRKPIWLSQMCSGREATLQDCPSGPWGKNTCNHDEDTWCECEDPDFDLRLVG
GDNLCSGRLEVLHKGVWGSVCDDNWGEKEDQVVCKQLGCGKSLSPSFRDRKCYGPGVGRIDL
DNVRCSGEEQSLEQCQHRFWGFHDCTHQEDVAVICSV

Signal sequence:

amino acids 1-15

Casein kinase II phosphorylation site.

amino acids 47-51, 97-101, 115-119, 209-213, 214-218, 234-238,
267-271, 294-298, 316-320, 336-340

N-myristoylation site.

amino acids 29-35, 43-49, 66-72, 68-74, 72-78, 98-104, 137-143,
180-186, 263-269, 286-292

Amidation site.

amino acids 196-200

Speract receptor repeated domain signature.

amino acids 29-67, 249-287

FIGURE 55

ACTGCACTCGGGTCTATCGATTGAATTCCCCGGGGATCCTCTAGAGATCCCTCGACCTCGAC
CCACCGTCCCGGACCGTGGCGGACCGTGGGCCGGTACCAAGGAAGAGTCTGCCGAAG
GTGAAGGCCATGGACTTCATCACCTCCACAGCCATCCTGCCCTGCTGTTGGCTGCCCTGGG
CGTCTCGGCCTTCCGGCTGCTGCAGTGGGTGCGGGAAAGGCCTACCTGCGGAATGCTG
TGGTGGTGATCACAGGCGCCACCTCAGGGCTGGCAAAGAATGTGCAAAAGTCTTCTATGCT
GCGGGTGCTAAACTGGTGCTCTGTGGCCGAATGGTGGGCCCTAGAAGAGCTCATCAGAGA
ACTTACCGCTCTCATGCCACCAAGGTGCAGACACACAAGCCTTACTGGTGACCTCGACC
TCACAGACTCTGGGCCATAGTTGCAGCAGCAGCTGAGATCCTGCAGTGCTTGGCTATGTC
GACATACTGTCAACAATGCTGGATCAGCTACCGTGGTACCATCATGGACACACCAGTGGA
TGTGGACAAGAGGGTCATGGAGACAAACTACTTGGCCCAGTTGCTCTAACGAAAGCACTCC
TGCCCTCCATGATCAAGAGGAGGCAAGGCCACATTGTCGCCATCAGCAGCATTCCAGGGCAAG
ATGAGCATTCTTTGATCAGCATATGCAGCCTCCAAGCACGCAACCCAGGCTTCTTGA
CTGTCTGCGTGCCGAGATGGAACAGTATGAAATTGAGGTGACCGTCATCAGCCCCGGCTACA
TCCACACCAACCTCTGTAAATGCCATCACCGGGATGGATCTAGGTATGGAGTTATGGAC
ACCACCCAGGCCAGGGCGAAGCCCTGGAGGTGGCCAGGATGTTCTGCTGCTGTGGG
GAAGAAGAAGAAAGATGTGATCCTGGCTGACTTACTGCCTCCTGGCTGTTATCTCGAA
CTCTGGCTCCTGGCTCTTCTTCAGCCTCATGGCCTCCAGGGCCAGAAAAGAGCGGAAATCC
AAGAACTCCTAGTACTCTGACCAGCCAGGGCAGGGCAGAGAACGAGCACTCTTAGGCTTGC
TTACTCTACAAGGGACAGTTGCATTGTTGAGACTTTAATGGAGATTGTCTACAAGTGGG
AAAGACTGAAGAACACATCTCGTGCAGATCTGCTGGCAGAGGACAATAAAAACGACAACA
AGCTTCTTCCCAGGGTGAGGGAAACACTTAAGGAATAATGGAGCTGGGTTAACACT
AAAAACTAGAAATAAACATCTCAAACAGTAAAAAAAAAAAAAGGGCGGCCGACTCTAG
AGTCGACCTGCAGAAGCTGGCCCATGGCCAATTGTTATTGCAGCTATAATGGTAC

FIGURE 56

MDFITSTAILPLLFGCLGVFGLFRLLQWVRGKAYLRNAVVTGATSGLGKEAKVFYAAGA
KLVLCGRNGGALEELIRELTASHATKVQTHKPYLVTFDLTDGAI
VAAAEEILQCFGYVDIL
VNNAGISYRGTIMDTTVDVDKRVMETNYFGPVALTKALLPSMIKRQGHIVAISSIQGKMSI
PFRSAYAASKHATQAFFDCLRAEMEQYEIEVTVISPGYIHTNLSVNAITADGSRYGVMDTTT
AQGRSPVEVAQDVLA AVGKKKDVLADLLPSLAVYLRTLAPGLFFSLMASRARKERKS KNS

Signal sequence:

amino acids 1-21

Transmembrane domain:

amino acids 104-120, 278-292

N-glycosylation site.

amino acids 228-232

Glycosaminoglycan attachment site.

amino acids 47-51

Casein kinase II phosphorylation site.

amino acids 135-139, 139-143, 253-257

Tyrosine kinase phosphorylation site.

amino acids 145-153, 146-153

N-myristoylation site.

amino acids 44-50, 105-111, 238-244, 242-248, 291-297

Amidation site.

amino acids 265-269

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 6-17

FIGURE 57

CCCACCGCGTCCGCTGGTGTAGATCGAGCAACCCCTCTAAAAGCAGTTAGAGTGGTAAAAAA
AAAAAAAAAACACACCAAACGCTCGCAGCCACAAAAGGGGATGAAATTCTCTGGACATCCTC
CTGCTTCTCCCGTTACTGATCGTCTGCTCCCTAGAGTCCTCGTGAAGCTTTTATTCTAA
GAGGAGAAAATCAGTCACCGCGAAATCGTGTGATTACAGGAGCTGGCATGGAATTGGGA
GAUTGACTGCCTATGAATTGCTAAACTAAAGCAAGCAGCTGGTCTCTGGATATAAATAAG
CATGGACTGGAGGAAACAGCTGCCAATGCAAGGGACTGGTGCCAAGGTTCATACCTTGT
GGTAGACTGCAGCAACCGAGAAGATATTACAGCTCTGCAAAGAAGGTGAAGGCAGAAATTG
GAGATGTTAGTATTTAGTAAATAATGCTGGTAGTCTATACATCAGATTGTTGCTACA
CAAGATCCTCAGATTGAAAAGACTTTGAAGTTAATGTACTTGACATTTCTGGACTACAAA
GGCATTCTCCTGCAATGACGAAGAATAACCATTGCCATATTGTCAGTGTGGCTCGGCAG
CTGGACATGTCTCGGTCCCCTTACTGGCTACTGTTCAAGCAAGTTGCTGCTGTTGGA
TTTCATAAAACTTGACAGATGAACTGGCTGCCTACAAATAACTGGAGTCAAAACAACATG
TCTGTGTCTTAATTCGTAACACTGGCTTCATCAAAATCCAAGTACAAGTTGGACCCA
CTCTGGAACCTGAGGAAGTGGTAAACAGGCTGATGCATGGATTCTGACTGAGCAGAAGATG
ATTTTATTCCATCTCTATAGCTTTTAACAACATTGAAAGGATCCTCCTGAGCGTT
CCTGGCAGTTAAAACGAAAATCAGTGTAAAGTTGATGCAGTTATTGGATATAAAATGA
AAGCGCAATAAGCACCTAGTTCTGAAAACTGATTACCAAGTTAGGGTATGTCATCTA
ATAGTGCAGAATTTAATGTTGAACCTCTGTTCTAATTATCCCCATTCTCAATA
TCATTTTGAGGCTTGGCAGTCTCATTACTACCACCTGTTCTTAGCCAAAAGCTGATT
ACATATGATATAAACAGAGAAACCTTAGAGGTGACTTAAGGAAAATGAAGAAAAGAA
CCAAAATGACTTATTAAAATAATTCCAAGATTATTGTGGCTCACCTGAAGGCTTGCAA
AATTGTACCATAACCGTTATTAAACATATTTTATTGATTGATGCACCTAAATTGTT
ATAATTGTGTTCTTTCTGTTCTACATAAAATCAGAAACTCAAGCTCTCTAAATAAAA
TGAAGGACTATATCTAGGGTATTCACAATGAATATCATGAACCTCAATGGTAGGTTTC
ATCCTACCCATTGCCACTCTGTTCTGAGAGATACTCACATTCAATGCCAAACATTCT
GCACAGGGAGCTAGAGGTGGATACACGTGTGCAAGTATAAAAGCATCACTGGATTAAAG
GAGAATTGAGAGAAATGTACCCACAAATGGCAGCAATAATAATGGATCACACTAAAAAAA
AAA
AAA

FIGURE 58

MKFLLDILLPLLIVCSLESFVKLFIPKRRKSVTGEIVLITGAGHGIGRLTAYEFAKLKSK
LVLWDINKHGLEETAACCKGLGAKVHTFVVDCSNREDIYSSAKKVKAEIFDVSI
LVNNAGVV
YTSDLFATQDPQIEKTFEVNVLAHFWTTKAFLPAMTKNNHGHIVTVASAAGHV
SVPFLLAYC
SSKFAAVGFHKTLTDELAALQITGVKTTCLCPNFVNTGFIKNPSTS
LGPTLEPEEVVNRLMH
GILTEQKMIFIPSSIAFLTTLERILPERFLAVLKRKISVKFDAVIGYKMKAQ

Signal sequence:

amino acids 1-19

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 30-34, 283-287

Casein kinase II phosphorylation site.

amino acids 52-56, 95-99, 198-202, 267-271

N-myristoylation site.

amino acids 43-49, 72-78, 122-128, 210-216

TOP SECRET//NOFORN

FIGURE 59

CCACCGCGTCCCGGACCGCGTGGTCGACTAGTTCTAGATCGCGAGCGGCCGCCCGCGCTC
AGGGAGGAGCACCGACTGCGCCGCACCCCTGAGAGATGGTGGTGCCATGTGGAAAGGTGATTG
TTTCGCTGGTCTGTTGATGCCCTGGCCCTGTGATGGCTGTTCGCTCCCTATAAGAAGT
GTTTCCATGCCACCTAACGGAGACTCAGGACAGCCATTATTCCTCACCCCTACATTGAAGC
TGGGAAGATCCA
AAAAGGAAGAGAATTGAGTTGGTCCGCCCCCTTCCCAGGACTGAACATGA
AGAGTTATGCCGGCTCCTCACCGTGAATAAGACTTACAACAGCAACCTCTCTGGTTC
TTCCCAGCTCAGATACAGCCAGAACGATGCCAGTAGTTCTGGCTACAGGGTGGCCGGG
AGGTTCATCCATGTTGGACTCTTGGAACATGGCCCTATGTTGTACAAGTAACATGA
CCTTGCCTGACAGAGACTTCCCCTGGACCACAACGCTCTCCATGCTTACATTGACAATCCA
GTGGGCACAGGGCTTCAGTTACTGATGATA
CCACGGGATTTACAGTGCACTAATTCA
GTTTTCCAGATA
TTCTGAATATAAAAATA
ATGACTTTATGTC
ACTGGGAGTCTTATGCAGGGAAATATGTGCCAGCCATTGCACACCTC
ATCCATTCCCTCAACCCCTGTGAGAGAGGTGAAGATCAACCTGAACGGAAATTGCTATTGGAGA
TGGATATTCTGATCCGAATCAATTATAGGGGCTATGCAGAATTCTGTACCAAATTGGCT
TGTGGATGAGAACGAAAAAGTACTCCAGAACGAGTGC
CATGAATGCATAGAACACATC
AGGAAGCAGAACTGGTTGAGGCCTTGAA
AAACTACTGGATAAAACTACTAGATGGC
GACTTAAC
AAGTGATCCTTCTTACTTCCAGAATGTTACAGGATGTAGTAATTACTATAACTTTGCGGT
GCACGGAACCTGAGGATCAGCTTACTATGTA
AAATTGGTCA
CTCCCAGG
GTGAGACAA
GCCATCCACGTGGGAATCAGACTTTAATGATGGA
ACTATAGTTGAAAGTACTTGC
GAGA
AGATACAGTACAGTCAGTTAAGCCATGGTTA
ACTGAA
ATCATGA
ATAATTATAAGGTTCTGA
TCTACAATGCCA
ACTGGACATCATCGTGGCAGCTGCC
CTGACAGG
ATGGACTGGAAAGGATCCCAGGA
ATACAAGAACGG
CAGAAAAAGTTGG
AAGATCTTAA
ATCTGACAGTGAAGTGGCTGGTTACATCCGGCAAGCGGGTGACTTCC
CATCAGGTAA
TTTAC
GAGGTGGAGGACATATT
TTACCC
TATGACCAGC
CTTGAGAGCTTTGACATGATTA
ATCGA
TTCA
TTTATGGAAAAGGATGG
GTT
ACTGG
GATA
AAACTAC
CTTCCC
AAAGAGAACAT
CAGAGG
TTTCATTGCT
GAAAAGAAA
ACTCG
AAAAACAGAAA
ATGTC
ATAGGA
ATA
TTA
TTCTTCA
ATCTGCA
AGATT
TTT
TTC
ATCA
AAAAATT
ATC
CTTG
AAACAAGT
GAGC
TTTG
TTT
GGGG
GAGATG
TTT
ACT
ACAA
ATT
AACAT
GAGT
ACAT
GAGT
AAGA
ATT
ACA
TTA
ACT
AAAGG
ATGG
GATG
TGA
ACT
GAG
ACA
AGAT
GT
ATA
AA
ATGA
AATT
TTAGGG
CTT
GAA
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GA
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TTT
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TGA
AAA
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TGC
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AG
CT
GTA
AC
AT
CTT
TCT
GCC
AA
TA
AC
AG
AA
GTT
GG
GAG
ATG
CT
CA
ATT
AT
CCC
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AA
AG
AA
ATT
CTT
GAA
ATA

FOOT 20' 24' 28' 32' 36' 40' 44' 48'

FIGURE 60

MVGAMWKIVSLVLLMPGCDGLFRSLYRSVSMPPKGDSGQPLFLTPYIEAGKIQKGREL
VGPPFPGLNMKSYAGFLTVNKTYNSNLFFWFFPAQIQPEDAPVVLWLQGGPGGSSMFGLFVEH
GPYVVTTSNMTLDRDFPWTTTLSMLYIDNPVGTGFSFTDDTHGYAVNEDDVARDLYSALIQF
FQIFPEYKNNDFYVTGESYAGKYVPAIAHLIHSNPNREVKINLNGIAIGDGYSDPESIIGG
YAEFLYQIGLLDEKQKKYFQKQCHECIEHIRKQNWFEEAFEILDKLLGDQLTSDPSYFQNV
CSNYYNFLRCTEPEDQLYYVKFLSLPEVRQAIHGNQTFNDGTIVEKYLREDTVQSVKPWLT
EIMNNYKVLIYNGQLDIIVAAALTERSLMGMDWKGSQEYKKAEEKVWKIFKSDSEVAGYIRO
AGDFHQVIIRGGGHILPYDQPLRAFDMINRFIYGKGWDPYVG

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 81-85, 132-136, 307-311, 346-350

Casein kinase II phosphorylation site.

amino acids 134-138, 160-164, 240-244, 321-325, 334-338, 348-352,
353-357, 424-428

Tyrosine kinase phosphorylation site.

amino acids 423-432

N-myristoylation site.

amino acids 22-28, 110-116, 156-162, 232-238

Serine carboxypeptidases, serine active site.

amino acids 200-208

Crystallins beta and gamma 'Greek key' motif signature.

amino acids 375-391

FIGURE 61

CGAGGGCTTCCGGCTCCGAATGGCACATGTGGGAATCCCAGTCTTGGCTACAACAT
TTTCCTTCTAACAAAGTCTAACAGCTGTTCTAACAGCTAGTGATCAGGGGTTCTTCTT
GCTGGAGAAGAAAGGGCTGAGGGCAGAGCAGGGCACTCTCACTCAGGGTACCAGCTCCTTG
CCTCTCTGTGGATAACAGAGCATGAGAAAAGTGAAGAGAGATGCAGCGGAGTGAGGTGATGGAAG
TCTAAAATAGGAAGGAATTGTGCAATATCAGACTCTGGGAGCAGTTGACCTGGAGAGC
CTGGGGAGGGCTGCTAACAAAGCTTCAAAAAACAGGAGCGACTTCACTGGCTGGGAT
AAGACGTGCCGGTAGGATAGGAAAGACTGGTTAGTCTTAATATCAAATTGACTGGCTGGG
TGAACCTAACAGCCTTTAACCTCTGGGAGATGAAAACGATGGCTTAAGGGGCCAGAAA
TAGAGATGCTTGTAAAATAAAATTAAAAGCAAGTATTATAGCATAAAGGCTAGA
GACCAAAATAGATAACAGGATTCCCTGAACATTCTAACAGGGAGAAAGTATGTTAAAATA
GAAAAACAAAATGCAGAAGGAGGAGACTCACAGAGCTAACCAACAGGAT~~T~~GGGACCCCTGGGTC
AGGCCAGCCTCTTGCTCCTCCGGAAATTATTTGGTCTGACCACCTGCCTGTGTTT
GCAGAATCATGTGAGGGCCAACCGGGGAAGGTTGGAGCAGATGAGCACACACAGGAGCCGTCT
CCTCACCGCCGCCCTCTCAGCATGGAACAGAGGCAGCCCTGGCCCCGGGCCCTGGAGGTGG
ACAGCCGCTCTGTGGTCTGCTCAGTGGCTGGGTGCTGCTGGCCCCCCCAGCAGCCGGC
ATGCCCTCAGTCAGCACCTTCACTCTGAGAATCGTGAUTGGACCTTCAACCACTTGACCGT
CCACCAAGGGACGGGGCCGTCTATGGGGGCCATCAACCGGGTCTATAAGCTGACAGGCA
ACCTGACCATCCAGGTGGCTATAAGACAGGGCCAGAAGAGGACAACAAGTCTCGTTACCG
CCCTCATCGTGCAGCCCTGAGCGAAGTGCTCACCCCTACCAACAATGTCACAAAGCTGCT
CATCATTGACTACTCTGAGAACCGCCTGCTGGCCTGTGGGAGCCTTACCAAGGGGTCTGCA
AGCTGCTGCCGCTGGATGACCTTTCATCCTGGTGGAGCCATCCCACAAGAAGGAGCACTAC
CTGTCCAGTGTCAACAAGACGGGCACCATGTACGGGTGATTGTGCGCTCTGAGGGTGAGGA
TGGCAAGCTTTCATGGCACGGCTGTGGATGGGAAGCAGGATTACTTCCGACCCGTCCA
GCCGGAAAGCTGCCCGAGACCCCTGAGTCCTCAGCCATGCTGACTATGAGCTACACAGCGAT
TTTGTCTCTCTCATCAAGATCCCTCAGACACCCCTGGCCCTGGTCTCCACTTGACAT
CTTCTACATCTACGGCTTGCTAGTGGGGCTTGTCTACTTCTCACTGTCCAGCCCGAGA
CCCTGAGGGTGTGGCCATCAACTCCGCTGGAGACCTCTTACACCTCACGCATCGTGC
CTCTGCAAGGATGACCCCAAGTCCACTCATACGTGCCCTGCCCTCGCTGCACCCGGG
CGGGGTGGAATACCGCCCTGAGGTGCTTACCTGGCCAAGCCTGGGACTCACTGGCCC
AGGCCTTCAATATCACCAAGCCAGGAGGATGTAUTCTTGCCTCTCTCAAAGGGCAGAAG
CACTATCACCAACCGCCCGATGACTCTGCCCTGTGCTTCCCTATCCGGGCCATCAACTT
GCAGATCAAGGAGCGCCTGCAGTCCTGCTACCAAGGGCAGGGCAACCTGGAGCTCAACTGGC
TGCTGGGAAGGACGCCAGTGCACGAAGGCGCTGTCCCCTCGATGATAACTTCTGTGGA
CTGGACATCAACCAGCCCTGGGAGGCTCAACTCCAGTGGAGGGCTGACCCCTGTACACCAC
CAGCAGGGACCGCATGACCTCTGTGGCCTCTACGTTACAACGGCTACAGCGTGGTTTG
TGGGGACTAAGAGTGGCAAGGCTGAAAAAGGTAAGAGTCTATGAGTTAGTCAAGTCCAATGCC
ATTCACCTCTCAGCAAAGAGTCCCTTGGAGGCTAGCTATTGGTGGAGATTAACTATAAG
GCAACTTATTTCTGGGAACAAAGGTGAAATGGGAGGTAAGAAGGGTTAATTTGTG
ACTTAGCTTCTAGCTACTTCCAGCCATCAGTCATTGGTATGTAAGGAATGCAAGCGTA
TTCAATATTCCAAACTTAAAGAAAAACTTAAAGAAGGTACATCTGCAAAAGCAAA

FIGURE 62

MGTLGQASLFAPPGNYFWSDHSALCFAESCEGQPGKVEQMSTHRSRLTAAPLSMEQRQPWP
RALEVDSRSVVLSSVVWVLLAPPAAGMPQFSTFHSENRDWTFNHLTVHQGTGAVYVGAINRV
YKLTKNLTIQVAHKTGPEEDNKSRYPPLIVQPCSEVLTLTNNVNKLIIIDYSENRLLACGSL
YQGVCKLLRLDDLFIILVEPSHKKEHYLSSVNKTGTMGYVIVRSEGEDGKLFIGTAVDGKQDY
FPTLSSRKLP RDPESSAMLDYELHSDFVSSLIKIIPSDTLALVSHFDIFYIYGFASGGFVYFL
TVQPETPEGVAINSAGDLFYTSRIVRLCKDDPKFH SYVSLPFGCTRAGVEYRLLQAAYLAKP
GDSL AQA FNITSQDDVLFAIFSKGQKQYHHPPDDSALCAFPIRAINLQIKERLQSCYQGEQN
LELNWLLGKD VQCTKAPVPIDDNF CGLDINQPLGGSTPVEGLTLYTTSRDRMTSVASYVYNG
YSVVFVGTKSGKLKKVRVYEFRCSNAIHLLSKE SLLEG SYWWRFNYRQLYFLGEQR

09604523-022004

Signal sequence:

amino acids 1-32

Transmembrane domain:

amino acids 71-87

N-glycosylation site.

amino acids 130-134, 145-149, 217-221, 381-385

Casein kinase II phosphorylation site.

amino acids 139-143, 229-233, 240-244, 291-295, 324-328, 383-387,
384-388, 471-475, 481-485, 530-534

N-myristoylation site.

amino acids 220-226, 319-325, 353-359, 460-466, 503-509

FIGURE 63

AGGCTCCCGCGCGGGCTGAGTGGACTGGAGTGGAAACCGGGTCCCCCGCTTAGAGAACACGCGATGACCA
CGTGGACCTCCGGCGAGGCCCGCACGCTGGACTCTGCTGGCTTGGCTTCTGGCTTCTGGCTCC
GCAGGCTGGACTGGAGCACCCCTGGCCCTCTGGCTCCGACATGACAGCTGGGCTGCAGGCCAAGGGCTGGA
ACTTCATGCTGGAGGATTCCACCTCTGGATCTTCGGGGCTCCATCCACTATTTCCGTGTGCCAAGGGAGTACT
GGAGGGACCGCCTGCTGAAGATGAAGGCTGTGGCTGAAACACCTCACCACTATGTTCCGTGGAACTCGCATG
AGCCAGAAAGAGGCAAATTGACTTCTCTGGAAACCTGGACCTGGAGGCTTCGCTCTGATGCCAGAGATCG
GGCTGTGGGTATTCTGCGTCAGGCCCTACATCTGAGTGGACCTCGGGGCTTGGCCAGCTGGCTAC
TCCAAGACCCCTGGCATGAGGCTGAGGACAACCTACAAGGGCTTACCGAAGCAGTGGACCTTATTGACCACC
TGATGTCCAGGGTGGTGCACCTCAGTACAAGCGTGGGGACCTATCATTGGCTGCAGGTGGAGAATGAATATG
GTTCTATAATAAAAGACCCCGCATACATGCCCTACGTCAAGAAGGCAGTGGAGGACCGTGGATTGTGGAACTGC
TCCTGACTTCAGACAAAGGATGGGCTGAGCAAGGGATTGTCCAGGGAGTCTGGCCACCATCAACTGCAGT
CAACACACGAGCTGCAGCTACTGACCACTTCTTCAACGTCCAGGGACTCAGCCCAGATGGTATGGAGT
ACTGGACGGGTGGTTGACTCGTGGGAGGCCCTCACAATATCTGGATTCTCTGAGGTTTGAAAACCGTGT
CTGCCATTGTGGACGCCGCTCCATCAACCTCTACATGTTCCACGGAGGACCAACTTTGGCTTCATGAATG
GAGCCATGCACTTCATGACTACAAGTCAGATGTACCAGCTATGACTATGATGCTGTGCTGACAGAAGCCGGCG
ATTACACGGCAAGTACATGAAGCTCGAGACTTCTGGCTCCATCTCAGGCATCCCTCCCTCCCCACCTG
ACCTTCTCCTCAAGATGCCGTATGCCCTTAACGCCAGTCTGTACCTGCTCTGTGGACGCCCTCAAGTACC
TGGGGAGCCAATCAAGTCTGAAAAGCCATCAACATGGAGAACCTGCCAGTCATGGGGAAATGGACAGTCCT
TCGGGTACATTCTCATGAGACCGACATCACCTCGTCTGCCATCCTCAGTGGCACGTGATGTCGGGGCAGG
TGTTTGTGAAACAGTATCCATAGGATTCTGGACTACAAGACAACGAAGATTGCTGTCCTCTGTATCCAGGGTT
ACACCGTGTGAGGATCTGGGAGAACCTGTTGAGTCAGTCAACTATGGGAGAATTATGATGACAGGCCAAAG
GCTTAATTGAAATCTCTATGAAATGATTCAACCCCTGAAAATCTCAGAATCTATAGCCTGGATATGAGAAAGA
GCTTCTTCAGAGGTTGGCTGGACAAATGGNNTTCCCTCCAGAAACACCCACATTACCTGCTTTCTTGTG
GTAGCTTGTCCATCAGCTCCACGCCCTGTGACACCTTCTGAAGCTGGAGGGCTGGAGAAGGGGTTGTATTCA
TCAATGCCAGAACCTGGACGTTACTGAAACATTGGACCCAGAAGACGCTTACCTCCAGGTCCCTGGTGA
GCAGCGGAATCAACCGGTACCGTCTTGTGAGGAGACGATGGGGGCCCTGCATTACAGTTACGGAAACCCCCC
ACCTGGGAGGAACCGTACATTAGTGGAGCGGTGGCACCCCTCCTGCTGGTGCAGTGGAGACTGCCGCC
CTCTTGACCTGAAGCCTGGTGTGCTGCCACCCCTACTGAAAAGCATCTCTTAAGTAGCAACCTCAGGG
ACTGGGGCTACAGTGTGCCCTGTCTCAGCTCAAACCTAAGCCTGAGGGAAAGGTGGGATGGCTCTGGGCC
TGGCTTTGTGATGATGGCTTCTACAGCCCTGCTTGTGCCAGGGCTGTCGGCTGTCTTAGGGTGGAGC
AGCTAATCAGATGCCAGCCTTGGCCTCAGAAAAAGTGTGAAACAGTGCCTTGCACCGAGCTCACAGCC
TGCAGGACATCTGCTGGACTCAGGCGTGTCTTGCTGGTCTGGGAGGCTTGGCACATCCCTCATGGCCCC
TTTATCCCCGAATCTGGGTGTGTCACCAGTGTAGAGGGTGGGAAGGGGTGTCACCTGAGCTGACTTTGTT
CTTCCCTCAACCTCTGAGCCTTCTTGGATTCTGGAAAGGAACCTGGCTGAGAACATGTGACTTCCCT
TCCCTCCACTCGTGTCTGGTGTCTAGTGGAGGACATGTGAGTCTGGCAGAAGCCATGCCCATGTCTGCA
CATCCAGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAAGCCATGGCCATGTCTGCA
AGGGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAAGCCATGGCCATGTCTGCA
GGAGGAGGACAGAACGGCCAGCTCACATGTGAGTCTGGCAGAAGCCATGGCCATGTCTGCA
ACAGAACGGCCAGCTCAGTGGCCCCGCTCCCCACCCCCCAGCCGAACAGCAGGGCAGAGCAGGCCCTCTC
GAAGTGTGTCAGTCCAGTCCGATTTGAGCCTTGTGTTCTGGGCCAGCCAAACACCTGGCTTGGCTACTGTCTGA
GTGCGAGTAAAGCTATAACCTGAACTACAA

FIGURE 64

MTTWSLRRR PARTLGLLLLVLGFLVLRRLDWSTLVPLRLHRQLGLQAKGWNFMLEDSTFW
IFGGSIHYFRVPREYWRDRLKMKACGLNTLTYVPWNLHEPERGKFDFSGNLDLEAFVLMA
AEIGLWVILRPGPYICSEMDLGGLPSWLLQDPGMRLRTTYKGFTEAVIDLYFDHLMMSRVVPLQ
YKRGGPIIAVQVENEYGSYNKDPAYMPYVKKALEDRGIVELLLTSNDNKGDSKGIVQGVLAT
INLQSTHELQLTTFLNVQGTQPKMVMEMWTGWFD SWGGPHNILD SSEVLKTVAIVDAGS
SINLYMFHGGTNFGFMNGAMHFHDYKSDVT SYDYDAVLTEAGDYTAKYMKLRDFFGSISGIP
LPPPDLLPKMPYEPLTPVLYLSLWDALKYLGEPIKSEKP INMENLPVNNGNGQSFYI LY
TSITSSGILSGHVHD RGQVFVNTVSIGFLDYKTTKIAVPLI QGYTVRL RILVENRGRVNYGEN
IDDQRKGLIGNLYLNDSP LKNFRIYS LDMKKSFFQRFGLDKWXSLPETPTLPAFFLGSL SIS
STPCDTFLKLEGWEKG VVFINGQNLGRYWNIGPQKTL YLPGPWLS SGINQVIVFEETMAGPA
LQFTETPHLGRNQYIK

Signal sequence:

amino acids 1-27

Casein kinase II phosphorylation site.

amino acids 141-118, 253-257, 340-344, 395-399, 540-544, 560-564

N-myristoylation site.

amino acids 146-152, 236-242, 240-246, 244-250, 287-293, 309-315,
320-326, 366-372, 423-429, 425-431, 441-447, 503-509, 580-586

FIGURE 65

GGGGACGCGGAGCTGAGAGGCTCCGGGCTAGCTAGGTGTAGGGGTGGACGGGTCAGGAGGCC
CTGGTGAGGGTCTCTACTTGGCCTTCGGTGGGGTCAAGACGCAGGCACCTACGCCAAAGG
GGAGCAAAGCCGGCTGGCCCCAGGACCTCCATCTCCAATGTTGGAGGAATC
CGACACGTGACGGTCTGTCCGCGTCTCAGACTAGAGGAGCGCTGTAAACGCCATGGCTCCC
AAGAAGCTGTCCCTGCCTCGTCCCTGCTGCTGCCGCTCAGCCTGACGCTACTGCTGCCCA
GGCAGACACTCGGTGTTGCTAGTGGATAGGGTCATGACCAGGTTCTCCTAGACGGGGCC
CGTTCCGCTATGTTGCTGGCAGCCTGCACTACTTCGGGTACCGGGGTGCTTGGGCCGAC
CGGCTTTGAAGATGCGATGGAGCGGCCTAACGCCATACAGTTATGTCCTGGAACTA
CCACGAGCCACAGCCTGGGTCTATAACTTAATGGCAGCCGGACCTCATGCCCTTCTGA
ATGAGGCAGCTAGCGAACCTGTTGGTCATACTGAGACCAGGACCTACATCTGTGAGAG
TGGGAGATGGGGGTCTCCATCTGGTGTGCTCGAAAACCTGAAATTGATCTAAGAACCTC
AGATCCAGACTCCTTGCGCAGTGGACTCCTGGTTCAAGGTCTGCTGCCAAGATATATC
CATGGCTTATACAATGGGGCAACATCATTAGCATTAGGTGGAGAATGAATATGGTAGC
TACAGAGCCTGTGACTTCAGCTACATGAGGCACTTGGCTGGCTTCCGTGACTGCTAGG
AGAAAAGATCTGCTCTCACACAGATGGCCTGAAGGACTCAAGTGTGGCTCCCTCCGGG
GACTCTATACCACTGTAGATTTGGCCCAGCTGACAACATGACCAAAATCTTACCCGCTT
CGGAAGTATGAACCCATGGGCCATTGGTAAACTCTGAGTACTACACAGGCTGGCTGGATT
CTGGGCCAGAATCACTCCACACGGTCTGTGTCAGCTGTAACCAAGGACTAGAGAACATGC
TCAAGTTGGGAGCCAGTGTGAACATGTACATGTTCCATGGAGGTACCAACTTGGATATTGG
AATGGTGCCATAAGAAGGGACGCTTCCGATTACTACAGCTATGACTATGATGCC
TATATCTGAAGCAGGGACCCACACCTAACGTTTGCTCTCGAGATGTCATCAGCAAGT
TCCAGGAAGTCTTGGACCTTACCTCCCCAGCCCCAAGATGATGCTTGGACCTGTG
ACTCTGCACCTGGTGGCATTACTGGCTTCCAGACTGCTTGGCTGGCCCCCAT
TCATTCAATCTGCCATGACCTTGAGGCTGTCAAGCAGGACCATGGCTCATGTTGACC
GAACCTATATGACCCATACCATTGAGCCAACACCATTGGGTGCAAATAATGGAGTC
CATGACCGTGCCTATGTGATGGTGGATGGGTGTTCCAGGGTGTGGAGCGAAATATGAG
AGACAAACTATTTGACGGGAAACTGGGGTCCAAACTGGATATCTGGTGGAGAACATGG
GGAGGCTCAGTTGGTCTAACAGCAGTGACTCAAGGGCTGTTGAAGCCACCAATTCTG
GGGCAAACAATCTTACCCAGTGGATGATGTTCCCTGAAAATTGATAACCTGTGAAGTG
GTGGTTCCCTCCAGTTGCCAAATGGCATATCTCAAGCTCTGGCCCCACATTCT
ACTCCAAAACATTCAATTAGGCTCAGTGGGACACATTCTATATCTACCTGGATGG
ACCAAGGGCAAGTCTGGATCAATGGTTAACCTGGCCGGTACTGGACAAAGCAGGGCC
ACAACAGACCCCTACGTGCCAAGATTCTGCTGTTCTAGGGAGCCCTAACAAAATTA
CATTGCTGGAACTAGAAGATGTACCTCTCCAGCCCCAAGTCCAATTGGATAAGCCTATC
CTCAATAGCACTAGTACTTGCACAGGACACATATCAATTCCCTTCAGCTGATACACTGAG
TGCCTCTGAACCAATGGAGTTAAGTGGGACTGAAAGGTAGGCCGGCATGGTGGCTCATGC
CTGTAATCCCAGCACTTGGGAGGCTGAGACGGGTGGATTACCTGAGGTCAAGGACTTCAAGA
CCAGCCTGGCCAACATGGTGAACACCGTCTCCACTAAAATACAAAAATTAGCCGGCGTG
ATGGTGGCACCCTCTAATCCCAGCTACTTGGGAGGCTGAGGGCAGGAGAATTGCTTGAATCC
AGGAGGGCAGAGGTTGCACTGAGTGGAGGTTGACCACTGCACTCCAGCCTGGCTGACAGTGA
GACACTCCATCTAAAAAAAAAA

FIGURE 66

MAPKKLSCLRSLLLPLSLLPQADTRSFVVDRGHDRFLLDGAPFRYVSGSLHYFRVPRVL
WADRLLKMRWSGLNAIQFYVPWNYHEPQPGVYNFNGSRDLIAFLNEAALANLLVILRPGPYI
CAEWEMGGLPSWLLRKPEIHLRTSDPDFLAAVDSWFVKLLPKIYPWLYHNGGNIIISIQVENE
YGSYRACDFSYMRHLAGLFRALLGEKILLFTTDGPEGLKCGSLRGLYTTVDFGPADNMTKIF
TLLRKYEPhGPLVNSEYYTGWLWQNHSTRVSATKGLENMLKLGA SVNM MYMF HGGTNF
GYWNGADKKGRFLPITTSYDYDAPISEAGDPTPKLFALRDVISKFQEVPPLGPLPPPSPKMML
GPVTLHLVGHLLAFLDLLCPRGPIHSILPMTFEAVKQDHGFMLYRTYMHTTIFEPTFWVPN
NGVHDRAYVMVDGVFQGVVERNMRDKLFLTGKLGSKLDILVENMGRSLFGSNSSDFKGLLKP
PILGQTILTQWMMFPLKIDNLVKWWFPLQLPKWPYPQAPSGPTFYSKTFPILGSVGDTFLYL
PGWTKGQVWINGFNLGRYWTKQGPQQTLYVPRFLLFPRGALNKITLLELEDVPLQPQVQFLD
KPILNSTSTLHRTHINSLSADETLSASEPMELSGH

Signal sequence:

amino acids 1-27

N-glycosylation site.

amino acids 97-101, 243-247, 276-280, 486-490, 625-629

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 4-8

Casein kinase II phosphorylation site.

amino acids 148-152, 234-238, 327-331, 423-427, 469-473, 550-554,
603-607, 644-648

Tyrosine kinase phosphorylation site.

amino acids 191-198

N-myristoylation site.

amino acids 131-137, 176-182, 188-194, 203-209, 223-229, 227-233,
231-237, 274-280, 296-300, 307-313, 447-453, 484-490

FIGURE 67

GCTTGAAACACGTCTGCAAGCCAAAGTTGAGCATCTGATTGGTTATGAGGTATTGAGTGC
ACCCACAATATGGCTTACATGTTGAAAAGCTTCTCATCAGTTACATATCCATTATTGTGT
TTATGGCTTATCTGCCTCTACACTCTCTGGTTATTCAGGATAACCTTGAAGGAATATT
CTTCGAAAAAGTCAGAGAAGAGAGCAGTTAGTGACATTCCAGATGTCAAAACGATTT
GCGTTCCCTTTCACATGGTAGACCAGTATGACCAGCTATATTCCAAGCGTTTGGTGTGTT
CTTGTCAAGAGTTAGTGAAAATAACTAGGGAAATTAGTTGAACCATGAGTGGACATTG
AAAAACTCAGGCAGCACATTCAACGCCAGGACAAGCAGGAGTTGCATCTGTTCATG
CTGTCGGGGGTGCCGATGCTGTCTTGACCTCACAGACCTGGATGTGCTAAAGCTTGAAC
AATTCCAGAAGCTAAAATTCTGCTAACAGATTCTCAAATGACTAACCTCCAAGAGCTCCACC
TCTGCCACTGCCCTGCAAAAGTTGAACAGACTGCTTTAGCTTCTCGCGATCACTTGAGA
TGCCTTCACGTGAAGTTCACTGATGTGGCTGAAATTCTGCCTGGGTGTATTGCTCAAAA
CCTTCGAGAGTTGACTTAATAGGCAATTGAACTCTGAAAACAATAAGATGATAGGACTTG
AATCTCTCCGAGAGTTGCCACCTTAAGATTCTCACGTGAAGAGCAATTGACCAAAGTT
CCCTCCAACATTACAGATGTGGCTCCACATCTAACAAAGTTAGTCATTATAATGACGGCAC
TAAACTCTGGTACTGAACAGCCTTAAGAAAATGATGAATGTCGCTGAGCTGGAACCTCCAGA
ACTGTGAGCTAGAGAGAATCCCACATGCTATTTCAGCCTCTAACAGGAACTGGAT
TTAAAGTCCAATAACATTGCCACAATTGAGGAAATCATCAGTTCCAGCATTAAAACGACT
GACTTGTAAATTATGGCATAACAAAATTGTTACTATTCCCTCCCTATTACCCATGTCA
AAAACTTGGAGTCACTTATTCTCAACAAACAGCTCGAACCTTACCGAGTGGAGTATT
AGTTACAGAAAACTCAGATGCTTAGATGTGAGCTACAACAAACATTCAATGATTCCAATAGA
AATAGGATTGCTTCAGAACCTGCAGCATTGCATATCACTGGAACAAAGTGGACATTCTGC
CAAAACAATTGTTAAATGCATAAAAGTTGAGGACTTGAATCTGGACAGAACTGCATCACC
TCACTCCCAGAGAAAGTTGGTCAGCTCTCCAGCTCACTCAGCTGGAGCTGAAGGGAACTG
CTTGGACCGCCTGCCAGCCAGCTGGGCCAGTGTGGATGCTCAAGAAAAGCGGGCTTGTG
TGGAAGATCACCTTTGATAACCCGCCACTCGAACGTCAAAGAGGCATTGAATCAAGACATA
AATATTCCCTTGCAAATGGATTAAACTAAGATAATATGCACAGTGATGTGCAGGAAC
AACTCCTAGATTGCAAGTGCTCACGTACAAGTTATTACAAGATAATGCATTAGGAGTAG
ATACATCTTTAAAATAACAGAGAGGGATGCATAGAAGGCTGATAGAAGACATAACTGAAT
GTTCAATGTTGAGGTTAAGTCATTCAAATCATTGTTTTTTCTTTGGGG
AAAGGAAAGGAAAATTATAACTAAATCTTGAATGCTTGTAAAGTAAATGATTAAATTGACATT
GCTGCCGCTACTGAATGTTACAAATTGCTGCCGTCAAAGTAAATGATTAAATTGACATT
TTCTTACTAAAAAAAAAAAAAA

FIGURE 68

MAYMLKKLLISYISIICVYGFICLYTLFWLFRIPLKEYSFEKVREESSFSDIPDVKNDFAFL
LHMVDQYDQLYSKRGVFLSEVSENKLREISLNHEWTFEKLRQHISRNAQDKQELHLFMLSG
VPDAVFDLTDLDVLKLELIPEAKIPAKISQMNTNLQELHLCHCPAKVEQTAFSFLRDHLRCLH
VKFTDVAEIPAIVYLLKNLRELYLIGNLNSENNKMIGLESLRELRLKILHVKSNLTKVPSN
ITDVAPHLTKLVIHNDGTKLVLNSLKKMMNVAELELQNCELERIPHAIIFSLSNLQELDLKS
NNIRTIEEIISFQHLKRRTCLKLWHNKIVTIPPSITHVKNLESLYFSNNKLESLPVAVFSLQ
KLRCLDVSYNNISMIPIEIGLLQNLQHLHITGNKVDILPKQLFKCIKLRTLNLGQNCITSLP
EKVGQLSQLTQLELKGNCLDRPAQLGQCRMLKKSGLVVEDHLFDTLPLEVKEALNQDINIP
FANGI

Digitized by srujanika@gmail.com

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 241-245, 248-252, 383-387

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 326-330

Casein kinase II phosphorylation site.

amino acids 48-52, 133-137, 226-230, 315-319, 432-436, 444-448

Tyrosine kinase phosphorylation site.

amino acids 349-355 375-381

N-myristoylation site.

amino acids 78-84, 124-130, 212-218, 392-398

FIGURE 69

CCCA CGCG TCGG CTTCTCTGGACTTGCATTCCATTCTTTCATGACAAACTGACTTTTTATTC
TTTTTCCATCTCTGGGCCAGCTGGATCCTAGGCCCTGGGAAGACATTGTGTTTACACACATAAGGAT
CTGTGTTGGGTTCTTCTCTCCCTGACATTGCATTGCTTAGTGGTTGTGTTGGGAGGGAGACCACGTGG
GCTCAGTGCTTGCTGCACTTATCTGCCTAGGTACATCGAAGTCTTGACCTCCATACAGTGAATTATGCCTGTC
ATCGCTGGTGGTATCTGGCGGCCCTGCTCTGCTGATAGTTGTCGTCTGTCTTACTTCAAAATACACAAC
GCGCTAAAAGCTGCAAAGGAACCTGAAGCTGTTGCTGTAAAAATCACAAACCCAGACAAGGTGTGGTGGGCCAAG
AACAGGCCAACCCATTGCCACGGAGCTTGCTCGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCCTCAA
AGTTTGATTCCCTGCCACCTGCTGCTGCGACATAAATGAGGGCTCTGAGTTAGGAAAGGCTCCCTCCTCAA
GCAGAGCCCTGAAGACTTCATGATGTCATGAGGGCACCTGTTGTGATGTCAGGACAGAAGAAAGGCACAG
CTCCCCATCAGTTCATGAAAATAACTCAGTGCTGGAACCCAGCTGCTGGAGATCCCCTACAGAGAGCTTC
CACTGGGGCAACCTTCAGGAAGGAGTTGGGGAGAGAGAACCCACTGTGGGAATGCTGATAAAACCAAGTCA
CACAGCTGCTCTATTCTCACACAAATCTACCCCTGCGTGGACTGACGTTCCCTGGAGGTGTCCAGAAA
GCTGATGTAACACAGAGCTATAAAAGCTGTCGGCTTAAGGCTGCCAGGCCCTGC~~AAAATGGAGCTTGT~~
AGAAGGCTCATGCCATTGACCCCTTAATTCTCTGTTGGCGAGCTGACAATGGCGAGGCTGAAGGCAAT
GCAAGCTGCACAGTCAGTCTAGGGGGTGC~~AAATATGGCAGAGACCCACAAGCCATGATCCTGCAACTCAATCCC~~
AGTGAGAACTGCACCTGGACAATAGAAAGACCAAGAAAACAAAGCATCAGAATTATCTTCTATGTCCAGCTT
GATCCAGATGGAAGCTGAAAGTGAACATTAAAGCTTGTGACCGAACCTCCAGCAATGGGCCCTGCTAGGG
CAAGTCTGCAGAAAAAGACTATGTCCTGATTTGAATCATCATCCAGTACATTGACGTTCAAAATAGTTACT
GAECTCAGCAAGAATTCAAAGAACTGTCCTTGCTTCTACTACTTCTCTCTAACATCTTCTATTCCAAACTGT
GGCGGTTACCTGGATACCTTGGAGGATCCTCACAGCCCAATTACCCAAAGCCGATCCTGAGCTGGCTTAT
TGTGTTGGCACATACAAGTGGAGAAAGATTACAAGATAAAACTAACTTCAAAGAGATTTCCTAGAAAATAGAC
AAACAGTGC~~AAATTGATTTCTTGC~~CATCTATGATGGCCCTCCACCAACTGCGCTGATTGGACAAGTCTGT
GGCGGTGTGACTCCCACCTTCGAATCGTCATCAAACCTCTGACTGTCGTGTTGTCTACAGATTATGCCAATTCT
TACCGGGGATTCTGCTTCTACACCTCAATTATGCAAGAAAACATCAACACTACATCTTAACTTGCTCTTCT
GACAGGATGAGAGTTATTATAAGCAAATCCTACCTAGAGGTTTAACTCTAATGGATAACTTGCAACTAAA
GACCCAACTTGAGACCAAAATTATCAAATGTTGGAATTCTGCTCCCTCTTAATGGATGTGGTACAATCAGA
AAGGTTAGAAGATCAGTCATTACTTACACCAATAATCACCTTCTGCATCCTCAACTCTGAAGTGTGATCACC
CGTCAGAAACAATCCAGATTATTGTAAGTGTGAAATGGGACATAATTCTACAGTGGAGATAATATACATAACA
GAAGATGATGTAATACAAAGTCAAATGCACTGGGAAATATAACACAGCATGGCTCTTTGAATCCAATTCA
TTTAAAAGACTATACTTGAATCACCATATTATGTTGGAATTGAAACCAACTCTTGTCAAGTTAGTCTGCAC
ACCTCAGATCCAAATTGTTGCTTCTTGATACCTGTAGAGCCTCCACCTCTGACTTGCATCTCCAAACC
TACGACCTAATCAAGAGTGGATGTAGTCGAGATGAAACTTGTAAAGGTGTATCCCTTATTGGACACTATGGGAGA
TTCCAGTTAATGCCCTTAAATTCTGAGAAGTATGAGCTGTGATCTGAGTGTAAAGTTGATATGTGAT
AGCAGTGACCACCAGTCGCTGCAATCAAGGTTGTGTCCTCAGAAGCAAACGGAGACATTCTCATATAATGG
AAAACAGATTCCATCATAGGACCCATTGCTGAAAAGGGATCGAAGTGCAGTGGCAATTCAAGGATTTCAGCAT
GAAACACATGCCAAGAAACTCCAAACCCAGCCTTCAACAGTGTGCACTGTTTCTCATGGTTCTAGCTCTG
AATGTGGTACTGTAGCGACAATCACAGTGAGGCATTGTAATCAACGGGAGACTACAAATACCAAGAAGCTG
CAGAACTATTAACTAACAGGTCCAACCCCTAAGTGAAGACATGTTCTCCAGGATGCCAAGGAAATGCTACCTCGT
GGCTACACATATTGAATAATGAGGAAGGGCCTGAAAGTGACACACAGGCCATGTA

FIGURE 70

MELVRLMPPTLLILSCLAEALMAEAEGNASCTVSLGGANMAETHKAMILQLNPSENCTWTI
ERPENKSIRIIIFSIVQLDPGSCESENIKVFDGTSSNGPLLGVCSKNDYVPVFESSSTLT
FQIVTDSARIQRTVVFYYFFSPNISIPNCGGYLDTLEGSFTSPNYPKPHPELAYCVWHIQV
EKDYKIKLNFKEIFLEIDKQCKFDLAIYDGPTNSGLIGQVGRVTPTFESSNSLTVVLS
TDYANSYRGFSASYTSIYAENINTTSLTCSSDRMRVIISKSYLEAFNSNGNNLQLKDPTCRP
KLSNVVEFSPVPLNGCGTIRKVEDQSIYTNIITFSASSTSEVITRQKQLQIIVKCEMGHNST
VEIIIYITEDDVIQSQNALGKYNTSMALFESNSFEKTILESPYYVDLNQTLFVQVSLHTSDPN
LVVFLDTCRASPTDFASPTYDLIKSGCSRDETCVYPLFGHYGRFQFNQFKFLRSMSSVYL
QCKVLICDSSDHQSRCNQGCVSRSKRDISSYWKTDSSIGPIRLKDRSASGNSGFQHETHA
EETPNQPFNSVHLFSFMVLALNVVTVATITVRHFVNQRADYKYQKLQNY

Signal sequence:

amino acids 1-24

Transmembrane domain:

amino acids 571-586

N-glycosylation site.

amino acids 29-33, 57-61, 67-71, 148-152, 271-275, 370-374,
394-398, 419-423

Casein kinase II phosphorylation site.

amino acids 22-26, 108-112, 289-293, 348-352, 371-375, 379-383,
408-412, 463-467, 520-524, 556-560

Tyrosine kinase phosphorylation site.

amino acids 172-180, 407-415, 407-416, 519-528

N-myristoylation site.

amino acids 28-34, 38-44, 83-89, 95-101, 104-110, 226-232

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 71

GACGGAAAGAACAGCGCTCCCGAGGCCGCGGAGCCTGCAGAGAGGACAGCCGGCCTGCGCCG
GGACATGCGGCCCAGGAGCTCCCAGGCTCGCCTGCCACAGCGCCACCGCCTGACCCCCACCTGGGAGTCC
TGCTGCCGCCGCCGTGCCCTGCCACAGCGCCACCGCCTGACCCCCACCTGGGAGTCC
CTGGACGCCGCCAGCTGCCCGCTGTTGACCAGGCCAAGTCGGCATCTCATCCACTG
GGGAGTGTTCCTCGTCCCCAGCTCGGTAGCGAGTGGTCTGGTGGTATTGGCAAAAGGAAA
AGATACCGAAGTATGTGAATTATGAAAGATAATTACCCCTCTAGTTCAAATATGAAGAT
TTTGGACCACTATTACAGCAAAATTTTAATGCCAACAGTGGGAGATATTTCAAGGC
CTCTGGTCCAATACATTGTCTTAACCTCCAAACATCATGAAGGCTTACCTTGTGGGGT
CAGAATATTGTGGAACCTGGATGCCATAGATGAGGGGCCAAGAGGGACATTGTCAAGGAA
CTTGAGGTAGCCATTAGGAACAGAACTGACCTGCGTTGGACTGTACTATTCCCTTTGA
ATGGTTTCATCCGCTTCTGAGGATGAATCCAGTTCAATTCCATAAGCGGCAATTCCAG
TTTCTAAGACATTGCCAGAGCTCTATGAGTTAGTGAACAACATCAGCCTGAGGTTCTGTGG
TCGGATGGTACGGAGGAGCACCGGATCAAACTGGAACAGCACAGGCTTCTGGCCTGGGTT
ATATAATGAAAGCCCAGTCCGGGCACAGTAGTCACCAATGATCGTTGGGAGCTGGTAGCA
TCTGTAAGCATGGTGGCTTCTACCTGCAGTGATCGTTATAACCCAGGACATTTTGCCA
CATAAATGGGAAAATGCATGACAATAGACAAACTGTCCTGGGCTATAGGAGGGAAAGCTGG
AATCTCTGACTATCTACAATTGAAGAATTGGTGAAGCAACTGTAGAGACAGTTCATGTG
GAGGAAATCTTGATGAATATTGGGCCACACTAGATGGCACCATTCCTGTAGTTTGAG
GAGCGACTGAGGCAAGTGGGCTGGCTAAAGTCAATGGAGAAGCTATTATGAAACCTA
TACCTGGCGATCCCAGAATGACACTGTCACCCAGATGTGTGGTACACATEAACGCTAAAG
AAAAATTAGTCTATGCCATTCTAAATGGGCCACATCAGGACAGCTGTTCTGGCCAT
CCCAAAGCTATTCTGGGGCAACAGAGGTGAAACTACTGGGCCATGGACAGCCACTTAACG
GATTCTTGAGAAAATGGCATTATGGTAGAACTGCCACAGCTAACCATTCAGATGC
CGTGTAAATGGGGCTGGCTCTAGCCCTAACTAATGTGATCTAAAGTGCAGCAGAGTGGCTG
ATGCTGCAAGTTATGCTAAGGCTAGGAACATCAGGTGTCTATAATTGTAGCACATGGAGA
AAGCAATGTAAACTGGATAAGAAAATTATTGGCAGTCAGCCCTTCCCTTTCCACTA
AATTCTTCTAAATTACCCATGTAACCATTAACTCTCCAGTGCACTTGCCATTAAAGTC
TCTTCACATTGATTGTTCCATGTGTGACTCAGAGGTGAGAATTTCACATTATAGTAG
CAAGGAATTGGTGGTATTATGGACCGAAGTAAAATTATGTTGAAGCCATATCCCCCATG
ATTATATAGTTATGCATCACTTAATATGGGATATTCTGGGAAATGCATTGCTAGTCAT
TTTTTTGTGCCAACATCATAGAGTGTATTACAAACCTAGATGGCATAGCCTACTACA
CACCTAATGTGTATGGTATAGACTGTTGCTCTAGGCTACAGACATATAAGCATGTTACTG
AATACTGTAGGCAATAGTAACAGTGGTATTGTATATCGAAACATATGGAAACATAGAGAAG
GTACAGTAAAATACTGTAAATAATGGTGCACCTGTATAGGGCACTTACCAAGAATGGAG
CTTACAGGACTGGAAGTTGCTCTGGGTGAGTCAGTGAGTGAATGTGAAGGCCTAGGACATTA
TTGAACACTGCCAGACGTTATAAAACTGTATGCTTAGGCTACACTACATTATAAAAAAAA
GTTTTCTTCTTCATTATAAAACATAAGTGTACTGTAACTTACAAACGTTTAATT
TTTAAACCTTTGGCTTTGTAATAACACTAGCTAAACATAACTCATTGTGCAA
ATGTAA

FIGURE 72

MRPQELPRLAFPLLLLLLPPPPCPAHSATRFDPWESLDARQLPAWFDQAKFGIFIHVG
VFSVPSFGSEWFWWYQKEKIPKYVEFMKDNYPPSFKYEDFGPLFTAKFFNANQWADIFQAS
GAKYIVLTSKHEGFTLWGSEYSWNNAIDEGPKRDIVKELEVAIRNRTDLRFLGLYYSLFEW
FHPLFLEDESSSFHKRQFPVSKTLPELYELVNYYQPEVLWSDGDGGAPDQYWNSTGFLAWLY
NESPVRGTVVTNDRWGAGSICKHGGFYTCSDRYNPGHLLPHKWENCMTIDKLSWGYRREAGI
SDYLTIEELVKQLVETVSCGGNLLMNIGPTLDGTISVVFEERLRQVGSWLKVNGEAIYETYT
WRSQNDTVTPDVWYTSKPKEKLVYAIFLKWPTSGQLFLGHPKAILGATEVKLLGHQPLNW
SLEQNGIMVELPQLTIHQMPCKWGWALALTNVI

Signal sequence:

amino acids 1-28

N-glycosylation site.

amino acids 171-175, 239-243, 377-381

Casein kinase II phosphorylation site.

amino acids 32-36, 182-186, 209-213, 227-231, 276-280, 315-319,
375-375

Tyrosine kinase phosphorylation site.

amino acids 361-369, 389-397

N-myristoylation site.

amino acids 143-149, 178-184, 255-261, 272-278, 428-434

Leucine zipper pattern.

amino acids 410-432

Alpha-L-fucosidase putative active site.

amino acids 283-295

FIGURE 73

AGCAGGGAAATCCGGATGTCTCGGTTATGAAGTGGAGCAGTGAGTGTGAGCCTAACATAGT
TCCAGAACTCTCCATCCGGACTAGTTATTGAGCATCTGCCTCTCATATCACCAAGTGGCCATC
TGAGGTGTTCCCTGGCTCTGAAGGGTAGGCACGATGCCAGGTGCTTCAGCCTGGTGTG
CTTCTCACTCCATCTGGACCACGAGGCTCTGGTCCAAGGCTCTTGCGTGAGAAGAGCT
TTCCATCCAGGTGTATGCAGAATTATGGGGATCACCCTTGTGAGCAAAAGGCGAACAGC
AGCTGAATTTCACAGAAGCTAAGGAGGCCTGTAGGCTGCTGGGACTAAGTTGGCCGGCAAG
GACCAAGTTGAAACAGCCTGAAAGCTAGCTTGAACACTGCAGCTATGGCTGGGTTGGAGA
TGGATTCGTGGTCATCTCTAGGATTAGCCCCAACCCCAAGTGTGGGAAAAATGGGGTGGGTG
TCCTGATTTGAAGGTTCCAGTGAGCCGACAGTTGCAGCCTATTGTTACAACTCATCTGAT
ACTTGGACTAACTCGTGATTCCAGAAATTATCACCAACCAAAGATCCCATAATTCAACACTCA
AACTGCAACACAAACAAACAGAATTATTGTCAAGTACAGTACCTACTCGGTGGCATCCCCTT
ACTCTACAATACCTGCCCTACTACTACTCCTCCTGCTCCAGCTTCCACTTCTATTCCACGG
AGAAAAAAATTGATTTGTGTCACAGAAGTTTATGAAACTAGCACCATGTCTACAGAAAC
TGAACCATTGTTGAAAATAAAGCAGCATTCAAGAATGAAGCTGCTGGGTTGGAGGTGTCC
CCACGGCTCTGCTAGTGCTCTCCTCTTCTTGGTGTGAGCTGGCTTGGATTTGC
TATGTCAAAAGGTATGTGAGGCCTTCCCTTACAAACAAGAATCAGCAGAAGGAAATGAT
CGAAACCAAAGTAGTAAAGGAGGAGAACGCCAATGATAGCAACCCATAATGAGGAATCAAAGA
AAACTGATAAAACCCAGAACAGAGTCCAAGAGTCCAAGCAAAACCTACCGTGGATGCCCTGGAA
GCTGAAGTTAGATGAGACAGAAATGAGGAGACACACCTGAGGCTGGTTCTTCATGCTCC
TTACCCCTGCCCTCAGCTGGGAAATCAAAGGCCAAAGAACCAAAGAAGAAAGTCACCCCTT
GGTTCTTAACGGAAATCAGCTCAGGACTGCCATTGGACTATGGAGTGCACCAAAGAGAATGC
CCTTCTCCTTATTGTAACCCCTGTCTGGATCCTATCCTCCTACCTCCAAAGCTTCCCACGGCC
TTCTAGCCTGGCTATGTCCTAATAATATCCACTGGAGAAAGGAGTTTGCAAAAGTGCAA
GGACCTAAACATCTCATCAGTATCCAGTGGTAAAAGGCCCTGGCTGTCTGAGGCTAGG
TGGGTTGAAAGCCAAGGAGTCAGTGAGACCAAGGCTTCTACTGATTCCGCAGCTCAGAC
CCTTCTCAGCTCTGAAAGAGAACACGTATCCCACCTGACATGTCCTCTGAGGCCGGTA
AGAGCAAAAGAATGGCAGAAAAGTTAGCCCTGAAAGCCATGGAGATTCTCATAACTGAG
ACCTAATCTCTGTAAGCTAAAATAAAGAAATAGAACAAAGCTGAGGATACGACAGTACACT
GTCAGCAGGGACTGTAACACACAGACAGGGTCAAAGTGTCTCTGAACACACATTGAGTTGGA
ATCACTGTTAGAACACACACACTTACTTTCTGGTCTCTACCACTGCTGATATTCTCT
AGGAAATATACTTTACAAGTAACAAAATAAAACTCTTATAAATTCTATTGATCTGA
GTTACAGAAATGATTACTAAGGAAGATTACTCAGTAATTGTTAAAAGTAATAAAATTCA
ACAAACATTGCTGAATAGCTACTATATGTCAAGTGCTGCAAGGTATTACACTCTGTAAT
TGAATATTATTCTCAAAAATTGCACATAGTAGAACGCTATCTGGAGCTATTGTTCT
GTTTGATATTCTAGCTTATCTACTTCCAAACTAATTGTTATTGAGACTAATCT
ATTCAATTCTCTAATATGGCAACCATTATAACCTTAATTATTAAACATACCTAACAG
TACATTGTTACCTCTATATACCAAAGCACATTAAAAGTGCCTTAACAAATGTATCACTA
GCCCTCCTTTCCAACAAGAAGGGACTGAGAGATGCAGAAATATTGTGACAAAAATTAA
AGCATTAGAAAATT

FIGURE 74

MARCFSLVLLTSIWTTRLLVQ GSLRAEELSIQVSCRIMGITLVSKKANQQLNFTEAKEACR
LLGLSLAGKDQVETALKASFETCSYGVGDGFVVISRISPNSPKCGKNGVGVLIWKPVSQF
AAYCYNSSDTWTNSCIPEIITTKDPIFNTQTATQTTEFIVSDSTYSVASPYSTIPAPTTTPP
APASTSIPRRKKLICVTEVFMETSTMSTETEPFVENKA AFKNEAGFGGVPTALLVLALLFF
GAAAGLGFCYVKRYVKAFPFTNKNQQKEMIETKVVKEEKANDSNPNEESKKTDKNPEESKSP
SKTTVRCLAEV

Signal sequence:

amino acids 1-16

Transmembrane domain:

amino acids 235-254

N-glycosylation site.

amino acids 53-57, 130-134, 289-293

Casein kinase II phosphorylation site.

amino acids 145-149, 214-218

Tyrosine kinase phosphorylation site.

amino acids 79-88

N-myristoylation site.

amino acids 23-29, 65-71, 234-240, 235-239, 249-255, 253-259

FIGURE 75

AGATGGCGGTCTTGGCACCTCAATTGCTCTCGTATTGGTGCACGACTTCACGATGG
CTCGCCCAACCTTACTACCTTCTGTCGGCCCTGCTCTGCTGCCTCCTACTCGTGAGGAA
ACTGCCGCCGCTCTGCCACGGTCTGCCACCCAACGCGAAGACGGTAACCGTGTGACTTG
ACTGGAGAGAAGTGGAGATCCTGATGTTCTCAGTGCATTGTGATGATGAAGAACCGCAGA
TCCATCACTGTGGAGCAACATATAGGCAACATTTCATGTTAGTAAAGTGGCAAACACAAT
TCTTTCTTCCGCTTGGATATTGCATGGCCTACTTACATCACACTCTGCATAGTGTCC
TGATGACGTGCAAACCCCCCTATATATGGGCCCTGAGTATATCAAGTACTTCAATGATAAA
ACCATTGATGAGGAACTAGAACGGACAAGAGGGTCAGTGGATTGTGGAGTTCTTGCAA
TTGGTCTAATGACTGCCAATCATTGCCCTATCTATGCTGACCTCTCCCTAAATACAAC
GTACAGGGCTAAATTTGGGAAGGTGGATGTTGGACGCTATACTGATGTTAGTACGGTAC
AAAGTGAGCACATCACCCTCACCAAGCAACTCCCTACCCCTGATCCTGTTCCAAGGTGGCAA
GGAGGCAATGCGCGGCCACAGATTGACAAGAAAGGACGGCTGTCTCATGGACCTCTCG
AGGAGAATGTGATCCGAGAATTAACTTAAATGAGCTATACCAGCGGCCAAGAAACTATCA
AAGGCTGGAGACAATATCCCTGAGGAGCAGCCTGTTCAACCCCCACACAGTGTCA
TGGGAAAACAAGAAGGATAAAGATCCTCACTTGGCAGTGCTCCTCTCCTGTCATT
CCAGGCTTTCCATAACCACAAGCCTGAGGCTGCAGCCTTNATTNATGTTTCCCTTG
CTGNGACTGGNTGGGCAGCATGCAGCTCTGATTTAAAGAGGCATCTAGGAATTGTCAG
GCACCCTACAGGAAGGCCTGCCATGCTGTTCAAGCTGGTCAGTGTGTTACTGCTTAC
TCATAGGACGGAGGGGGAAATGGTTCCCTCCAAGCTGGTCAGTGTGTTACTGCTTATC
AGCTATTAGACATCTCCATGGTTCTCCATGAAACTCTGTGGTTCATCATTCTCTTAG
TTGACCTGCACAGCTGGTTAGACCTAGATTTAACCTAAGGTAAGATGCTGGGTATAGAA
CGCTAAGAATTTCACCAAGGACTCTGCTTCTTAAGCCCTCTGGCTCGTTATGGTC
TTCATTAAAGTATAAGCCTAACTTGTGCTAGTCCTAAGGAGAAACCTTAACCACAAAG
TTTTTATCATTGAAGACAATATTGAACAACCCCTATTTGTGGGATTGAGAAGGGGTGAA
TAGAGGCTTGAGACTTCCCTTGTGGTAGGACTTGGAGGAGAAACCCCTGGACTTCAC
TAACCCCTGACATACTCCCCACACCCAGTTGATGGCTTCCGTAATAAAAGATTGGATT
TCCTTTG

FIGURE 76

MAVLAPLIALVYSVPRLSRWLAQPYYLLSALLSAAFLLVRKLPPCHGLPTQREDGNPCDFD
WREVEILMFLSAIVMMKNRRSITVEQHIGNIFMF SKVANTILFFRLDIRMGLLYITLCIVFL
MTCKPPLYMGPEYIKYFNDKTIDEELERDKRVTWIVEFFANWSNDCQSFAPIYADLSLKYNC
TGLNFGKVDVGRYTDVSTRYKVSTSPLTKQLPTLILFQGGKEAMRRPQIDKKGRAVSWTFSE
ENVIREFNLNELYQRACKLSKAGDNIPEEQPVASTPTTVSDGENKKDK

Signal sequence:

amino acids 1-48

Transmembrane domain:

amino acids 111-125

N-glycosylation site.

amino acids 165-169, 185-189

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 154-158, 265-269

Casein kinase II phosphorylation site.

amino acids 51-55, 145-149, 245-249, 286-290, 288-292

N-myristoylation site.

amino acids 188-194, 225-231

Myb DNA-binding domain repeat signature 1.

amino acids 244-253

FIGURE 77

GGACAGCTCGCGCCCCGAGAGCTAGCCGTCGAGGAGCTGCCTGGGACGTTGCCCTG
GGGCCCCAGCCTGGCCGGGTCAACCTGGCATGAGGAGATGGCCTGTTGCTCCTGGTCCA
TTGCTCCTGCTGCCCGCTCCTACGGACTGCCCTCTACAACGGCTCTACTACTCCAACAG
CGCCAACGACCAGAACCTAGGCAACGGTCAAGGCAAAGACCTCCTTAATGGAGTGAAGCTGG
TGGTGGAGACACCCGAGGAGACCCCTGTTCACCTACCAAGGGCCAGTGTGATCCTGCCCTGC
CGCTACCGCTACGAGCCGGCCCTGGTCTCCCCGGCGGTGTGCGTGTCAAATGGTGGAAAGCT
GTGGAGAACGGGCCCCAGAGAAGGACGTGCTGGTGGCCATCGGCTGAGGCACCGCTCCT
TTGGGACTACCAAGGCCGCGTGCACCTGCGGCAGGACAAAGAGCATGACGTCTCGCTGGAG
ATCCAGGATCTGCGGCTGGAGGACTATGGCGTTACCGCTGTGAGGTCAATTGACGGCTGGA
GGATGAAAGCGGTCTGGTGGAGCTGGAGCTGCGGGGTGTGGCTTTCTTACCAAGTCCCCA
ACGGCGCTACCAGTCAACTCCACCGAGGGCCAGCAGGTCTGTGCAGAGCAGGCTGCGGTG
GTGGCCTCCTTGAGCAGCTCTCCGGGCCTGGGAGGAGGGCCTGGACTGGTGCAACGCGGG
CTGGCTGCAGGATGCTACGGTGCAGTACCCCATCATGTTGCCCGCAGCCCTGCGGTGGCC
CAGGCCTGGCACCTGGCGTGCAGCTACGGCCCCGCCACCGCCGCTGCACCGCTATGAT
GTATTCTGCTTCGCTACTGCCCTCAAGGGCGGGTGTACTACCTGGAGCACCTGAGAAGCT
GACGCTGACAGAGGCAAGGGAGGCCTGCCAGGAAGATGATGCCACGATGCCAAGGTGGAC
AGCTCTTGCCGCCTGGAAGTCCATGGCCTGGACCGCTGCGACGCTGGCTGGCTGGCAGAT
GGCAGCGTCCGCTACCCGTGGTCACCCGATCCTAACTGTGGGCCCCAGAGCCTGGGTT
CCGAAGCTTGGCTCCCCGACCCGAGAGCCGCTTGTACGGTGTAACTGCTACCGCCAGC
ACTAGGACCTGGGCCCTCCCTGCCGCATTCCCTACTGGCTGTGTATTATTGAGTGGTT
CGTTTCCCTGTGGGTTGGAGCCATTAACTGTTTATACTTCTCAATTAAATTCT
TTAACATTTTTACTATTTTGTAAGCAAACAGAACCCATGCCCTTGTGCTCCTG
GATGCCCACTCCAGGAATCATGCTGCTCCCTGGCCATTGCGGTTTGTGGCTTCTG
GAGGGTCCCCGCCATCCAGGCTGGTCTCCCTCCCTTAAGGAGGTTGGTGCAGAGTGGG
GGTGGCCTGTCTAGAATGCCGCCGGAGTCCGGCATGGTGGCACAGTCTCCCTGCCCT
CAGCCTGGGGAAGAAGAGGGCCTGGGGCCTCCGGAGCTGGCTTGGCCTCTCCTGCC
CACCTCTACTCTGTGAAGCCGCTGACCCAGTCTGCCACTGAGGGCTAGGGCTGGAA
GCCAGTTCTAGGCTCCAGGCAGAACATCTGAGGGAAAGGAAGAAACTCCCCTCCCCGTTCC
TCCCTCTCGGTTCCAAAGAACATCTGTTGTGTCATTGTTCTCCTGTTCCCTGTGTGG
GGAGGGGCCCTCAGGTGTGTACTTGGACAATAATGGTGCTATGACTGCCCTCCGCCAA
AA
AA

FIGURE 78

MGLLLVPLLLPGSYGLPYNGFYYSNSANDQNLGNHGKDLLNGVKLVVETPEETLFTYQ
GASVILPCRYRYEPALVSPRRVRVKWWKLSENGAPEKDVLAIGLRHRSFGDYQGRVHLRQD
KEHDVSLEIQDLRLEDYGRYRCEVIDGLEDESGLVELELRGVVFQSPNGRYQFNFHEGQQ
VCAEQAAVVASFEQLFRAWEEGLDWCNAGWLQDATVQYPIMLPRQPCGGPGLAPGVRSYGP
HRRLHRYDVFCFATALKGRVYYLEHPEKLTLTEAREACQEDDATIAKVGQLFAAWKFHGLDR
CDAGWLADGSVRYPVVHPHPNCGPPEPGVRSFGFPDPQSRLYGVYCYRQH

Signal sequence:

amino acids 1-17

Casein kinase II phosphorylation site.

amino acids 29-33, 53-57, 111-115, 278-282

Tyrosine kinase phosphorylation site.

amino acids 137-145

N-myristoylation site.

amino acids 36-42, 184-190, 208-214, 237-243, 297-303, 307-313

T05220-20251-0660

FIGURE 79

GGAGAGCGGAGCGAAGCTGGATAACAGGGGACCG**ATG**ATGTGGCGACCATCAGTTCTGCTGC
TTCTGTTGCTACTGAGGCACGGGGCCAGGGGAAGCCATCCCCAGACGCAGGCCCTCATGGC
CAGGGGAGGGTGCACCAGGGGGCCCCCTGAGCGACGCTCCCCATGATGACGCCAACGGAA
CTTCCAGTACGACCATGAGGCTTCCTGGACGGGAAGTGGCCAAGGAATTGACCAACTCA
CCCCAGAGGAAAGCCAGGCCGTCTGGGCGGATCGTGGACCGCATGGACCGCGCGGGGAC
GGCGACGGCTGGGTGTCGCTGGCCGAGCTCGCGCGTGGATCGCGCACACGCAGCAGCGCA
CATACGGGACTCGGTGAGCGCGGCCTGGACACGTACGACACGGACCGCGACGGCGTGTGG
GTTGGAGGAGCTGCGCAACGCCACCTATGCCACTACGCCCTGGTGAAGAATTGAC
GTGGAGGATGCAGAGACCTACAAAAAGATGCTGGCTGGACGAGCGCGTGGTGAAGAATTGAC
CGACCAAGGATGGGACTCGATGCCACTCGAGAGGAGCTGACAGCCTTGCACCCGAGG
AGTCCCTCACATGCGGACATCGTATTGCTGAAACCCCTGGAGGACCTGGACAGAAACAAA
GATGGCTATGTCCAGGTGGAGGAGTACATCGCGGATCTGTACTCAGCCGAGCCTGGGAGGA
GGAGCCGGCGTGGTGCAGACGGAGAGGCAGCAGTCCGGACTTCCGGATCTGAACAAGG
ATGGGCACCTGGATGGAGTGAGGTGGCCACTGGTGCTGCCCTGCCAGGACCAAGCCC
CTGGTGGAAAGCCAACCACCTGCTGCACGAGAGCGACACGGACAAGGATGGCGGCTGAGCAA
AGCGGAAATCCTGGTAATTGAAACATGTTGTGGCAGTCAGGCCACCAACTATGGCGAGG
ACCTGACCCGGCACACGATGAGCTG**TGAG**CACCGCGCACCTGCCACAGCCTCAGAGGCCCG
CACAAATGACCGGAGGAGGGCCGCTGGTCTGGCCCTCCCTGTCCAGGGCCCGCAGGAG
GCAGATGCAGTCCCAGGCATCCTGCCCTGGCTCTCAGGGACCCCTGGTCGGCTTC
TGTCCCTGTACACCCCCAACCCAGGGAGGGCTGTCATAGTCCCAGAGGATAAGCAATAC
CTATTCTGACTGAGTCTCCAGCCCAGACCCAGGGACCCCTGGCCCAAGCTCAGCTCTAA
GAACCGCCCCAACCCCTCCAGCTCAAATCTGAGCCTCCACCATAGACTGAAACTCCCT
GGCCCCAGCCCTCTGCCTGGCCTGGACACCTCCTCTGCCAGGAGGAATAA
AAGCCAGCGCCGGGACCTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAA

DOCT410669
2024-02-28

FIGURE 80

MMWRPSVLLLLLRLHGAQGKPSPDAGPHQGRVHQAAAPSLDAPHDDAHGNFQYDHEAFLGR
EVAKEFDQLTPEESQARLGRIVDRMDRAGDGWVSLAELRAWIAHTQQRHIRDSVSAAWDT
YDTDGRVGWEELRNATYGHYAPGEFHDVEDAETYKKMLARDERRFRVADQDGDSMATRE
ELTAFLHPEEFPHMRDIVIAETLEDLDRNKGYVQVEEYIADLYSAEPGEEEPAWVQTERQQ
FRDFRDLNKDGHLDGSEVGHVLPPAQDQPLVEANHLLHESDTDKDGRLSKAEILGNWNMFV
GSQATNYGEDLTRHHDEL

Signal sequence:

amino acids 1-20

N-glycosylation site.

amino acids 140-144

Casein kinase II phosphorylation site.

amino acids 72-76, 98-102, 127-131, 184-188, 208-212, 289-293,
291-295, 298-302

N-myristoylation site.

amino acids 263-269, 311-317

Endoplasmic reticulum targeting sequence.

amino acids 325-330

FIGURE 81

GGGGCCTTGCCTCCGCACTCGGGCGCAGCCGGGTGGATCTGAGCAGGTGCGGAGCCCCGG
GCGGCAGGGCGCGGGTGCAGGGGATCCCTGACGCCCTGTCCCTGTTCTTCGCTCCCAG
CCTGTCTGTCGCTGTTGGCGCCCCGCCTCCCGCGGTGCGGGGTTGCACACCGATCCTG
GGCTTCGCTCGATTGCCCGAGGGCGCTCCCAGACCTAGAGGGGCGCTGGCCTGGAGCAG
CGGGTCGTCGTTCTCTCCCTGCGCCGCCCGGGATCCGAAGGGTGCGGGGCTCT
GAGGAGGTGACCGCGGGGCTCCCGCACCTGGCCTGCCGCATTCTCCCTCTCCAG
GTGTGAGCAGCCTATCAGTCACCATGTCCGCAGCCTGGATCCCGCTCTCGGCCTCGGTGTG
TGTCTGCTGCTGCCGGGCCCGGGCAGCGAGGGAGCCGCTCCCATTGCTATCACATG
TTTACACAGAGGCTTGGACATCAGGAAAGAGAACAGCATGTCCTCTGCCAGGGGCTGCC
CTCTTGAGGAATTCTCTGTGTATGGGAACATAGTATGCTCTGTATCGAGCATATGTGGG
GCTGCTGTCACAGGGAGTAATCAGCAACTCAGGGGACCTGTACGAGTCTATAGCCTACC
TGGTCGAGAAAACATTCCCTCAGTAGATGCCAATGGCATCCAGTCTCAAATGCTTCTAGAT
GGTCTGCTCTTACAGTAACAAAGGCAAAGTAGTACACAGGAGGCCACAGGACAAGCA
GTGTCCACAGCACATCCACCAACAGGTAAACGACTAAAGAAAACCCGAGAAGAAAACGG
CAATAAAGATTGTAAGCAGACATTGCATTTCTGATTGATGGAAGCTTAATATTGGCAGC
GCCGATTTAATTACAGAAGAATTGGGAAAGTGGCTCTAATGTTGGGAAATTGGAAACA
GAAGGACCACATGTGGCCTTGTCAAGCCAGTGAACATCCAAAATAGAATTTCAGGGG
AAACTTACATCAGCAAAGATGTTGTTGCCATAAGGAAGTAGGTTCAAGGGGTA
ATTCCAATACAGGAAAAGCCTGAAGCATACTGCTCAGAAATTCTCAGGGTAGATGCTGGA
GTAAGAAAAGGGATCCCAAAGTGGTGGTATTATTGATGGTGGCCTCTGATGACAT
CGAGGAAGCAGGCATTGTGGCAGAGAGTTGGTGTCAATGTATTAGTTCTGTGGCCA
AGCCTATCCCTGAAGAACTGGGATGGTCAGGATGTCACATTGTTGACAAGGCTGTCTG
CGGAATAATGGCTTCTCTTACACATGCCCAACTGGTTGGCACCACAAAATACGTAAA
GCCTCTGGTACAGAACGCTGTGCACTCATGAACAAATGATGTGCAAGACCTGTTAACT
CAGTGAACATTGCCCTCTAATTGATGGCTCCAGCAGTGTGGAGATAGCAATTCCGCC
ATGCTTGAATTGTTCCAACATAGCCAAGACTTTGAAATCTGGACATTGGTGCCAGAT
AGCTGCTGTACAGTTACTTATGATCAGCGCACGGAGTTCACTGACTATAGCACCA
AAGAGAATGTCCTAGCTGTCACTAGAAACATCCGCTATATGAGTGGTGGAACAGCTACTGG
GATGCCATTCCCTCACTGTTAGAAATGTGTTGGCCCTATAAGGGAGAGGCCAACAGAA
CTTCCTAGTAATTGTCACAGATGGGAGTCCTATGATGATGTCAGGCTGAGCTGCTG
CACATGATGCAGGAATCACTATCTCTGTGTTGGTGGCTGGCACCTCTGGATGACCTG
AAAGATATGGCTCTAAACCGAAGGAGTCTCAGCCTTCTTACAAGAGAGTTCAAGGATT
AGAACCAATTGTTCTGATGTCATCAGAGGCATTGTAGAGATTCTTAGAATCCAGCAAATGG
TAACATTGACAACTGAAAGAAAAAGTACAAGGGGATCCAGTGTGAAATTGTATT
CTCATAATACTGAAATGCTTACTGATCAGATACAAAATATTAGTATGTCAAC
AGCCATTAGGCAAATAAGCACTCCTTAAAGCCGCTGCCTCTGGTTACAATTACAGTGT
ACTTTGTTAAAACACTGCTGAGGCTTCATAATCATGGCTCTAGAAACTCAGGAAAGAGGA
GATAATGTGGATTAAAACCTTAAGAGTTCTAACCATGCCTACTAAATGTACAGATATGCAA
TTCCATAGCTCAATAAGAATCTGATACTTAGACCAAAAAAAA

065470-25470-065470

FIGURE 82

MSAAWIPALGLGVCLLLLPGPAGSEGAAPIAITCFTRGLDIRKEKADVLCPGGCPEEFSVY
GNIVYASVSSICGAAVHRGVISNSGGPVRYSLPGRENYSSVDANGIQSQMLSRWSASFTVT
KGKSSTQEATGQAVSTAHPPTGKRLKKTPEKKTGNKDCKADIAFLIDGSFNIQQRNFNLQKN
FVGKVALMLGIGTEGPHVGLVQASEHPKIEFYLNFTSAKDVLFAIKEVGFRGGNSNTGKAL
KHTAQKFFTVDAGVRKGIPKVVVFIDGWPSSDIEEAGIVAREFGVNVFIVSVAKPIPEELG
MVQDVTFVDKAVCRNNGFFSYHMPNWFGTTKYVKPLVQKLCTHEQMMCSKTCYNSVNIAFLI
DGSSSVGDSNFRMLFEVSNIAKTFEISDIGAKIAAVQFTYDQRTESFTDYSTKENVLAVI
RNIRYMSGGTATGDAISFTVRNVFGPIRESPNKNFLVIVTDGQSYDDVQGPAAAHDAGITI
FSVGVAWAPLDDLKDMASKPKESHAFFTREFTGLEPIVSDVIRGICRDFLESQQ

TOP 2000 PROTEINS

Signal sequence:

amino acids 1-24

N-glycosylation site.

amino acids 100-104, 221-225

Casein kinase II phosphorylation site.

amino acids 102-106, 129-133, 224-228, 316-320, 377-381, 420-424,
425-429, 478-482, 528-532

N-myristoylation site.

amino acids 10-16, 23-29, 81-87, 135-141, 158-164, 205-211,
239-245, 240-246, 261-267, 403-409, 442-448, 443-449

Amidation site.

amino acids 145-149

FIGURE 83

CGCCCGCGCTCCCGCACCGCGGCCGCCACCGCGCCGCTCCGCATCTGCACCCGCAGCCC
GGCGGCCTCCCGCGGGAGCGAGCAGATCCAGTCAGTCCGGCCCGCAGCGCAACTCGGTCCAGTCG
GGCGCGGGCTGCGGGCGCAGAGCGGAGATGAGCGGGCTTGGGCCACCCCTGCTGTGCCTGC
TGCTGGCGGCCGGCGTCCCCACGGCCCCCGCGCCGCTCCGACGGCGACCTCGGCTCCAGTC
AAGCCCGGCCGGCTCTCAGCTACCCGAGGAGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
GGTTGAGGAAGTGTGGAGGACACGCAGCACAAATTGCGCAGCGCGTGGAAAGAGATGGAGG
CAGAAGAACGCTGCTGCTAAAGCATCATCAGAAGTGAACCTGGCAAACATTACCTCCCAGCTAT
ACAATGAGACCAACACAGACACGAAGGTTGAAATAATACCATCCATGTGCACCGAGAAAT
TCACAAGATAACCAACAACCAGACTGGACAAATGGTCTTTCAGAGACAGTTATCACATCTG
TGGGAGACGAAGAAGGCAGAAGGAGCAGGACTGTGCATCATCGACGAGGACTGTGGGCCAGC
ATGTAUTGCCAGTTGCCAGCTTCCAGTACACCTGCCAGCCATGCCGGGCCAGAGGATGCT
CTGCACCCGGGACAGTGAGTGCTGTGGAGACCAGCTGTGCATCATCGACGAGGACTGTGGGCCAGC
TGGCCACCAGGGGCAGCAATGGGACCATCTGTGACAACCAGAGGGACTGCCAGCCGGGCTG
TGCTGTGCCTCCAGAGAGGGCTGCTGTTCCCTGTGTGCACACCCCTGCCGTGGAGGGCGA
GCTTGCCATGACCCGCCAGCCGGCTCTGGACCTCATCACCTGGAGCTAGAGCCTGATG
GAGCCTTGGACCGATGCCCTTGTGCCAGTGGCCTCCTGCCAGCCCCACAGCCACAGCCTG
GTGTATGTGTGCAAGCCGACCTTGTGGGGAGCCGTGACCAAGATGGGAGATCCTGCTGCC
CAGAGAGGTCCCCGATGAGTATGAAGTTGCCAGCTCATGGAGGAGGTGCCAGGGAGCTGG
AGGACCTGGAGAGGGAGCCTGACTGAAGAGATGGCGCTGGGGAGCCTGCCGTGCCGCGCT
GCACTGCTGGAGGGAGAGATTTAGATCTGGACCCAGGGCTGTGGTAGATGTGAAATAGAA
ATAGCTAATTATTCCCCAGGTGTGCTTAGGCGTGGCTGACCAGGCTTCTCCTACA
TCTTCTTCCCAGTAAGTTCCCCTCTGGCTTGACAGCATGAGGTGTTGTGCATTGTCAGC
TCCCCCAGGCTGTTCTCAGGCTCACAGTCTGGTGTGGAGAGTCAGGCAGGGTTAAC
TGCAGGAGCAGTTGCCACCCCTGTCCAGATTATTGGCTGCTTGCCTCTACAGTTGGCAG
ACAGCCGTTGTTCTACATGGCTTGATAATTGTTGAGGGAGGAGATGGAAACAATGTGG
AGTCTCCCTGTGATTGGTTGGGAAATGTGGAGAAGAGTGCCTGCTTGCAAAACATCAA
CCTGGCAAAATGCAACAAATGAATTTCACCGCAGTTCTTCCATGGCATAGGTAAGCTG
TGCCTTCAGCTGTTGAGATGAAATGTTCTGTTCACCCGCATTACATGTGTTATTCC
AGCAGTGTGCTCAGCTCTACCTCTGTGCCAGGGCAGCATTTCATATCCAAGATCAATT
CCTCTCTCAGCACAGCCTGGGGAGGGGTCTTGTCTCCTCGTCCATCAGGGATCTCAGAG
GCTCAGAGACTGCAAGCTGCTGCCAAGTCACACAGCTAGTGAAGACAGAGCAGTTCT
CTGGTTGTGACTCTAACGCTCAGTGCTCTCCACTACCCACACCAGCCTGGTGCCACCAA
AAGTGCTCCCCAAAAGGAAGGAGAATGGATTGGCTTGAGGCATGCACATCTGGAATTAA
GTCAAACATATTCTCACATCCCTCTAAAGTAAACTACTGTTAGGAACAGCAGTGTCTCAC
AGTGTGGGGCAGCCGTCTTAATGAAGACAATGATATTGACACTGTCCCTTTGGCAGT
TGCATTAGTAACCTTGAAAGGTATATGACTGAGCGTAGCATAAGGTTAACCTGCAGAAACA
GTACTTAGGTAATTGTAGGGCGAGGATTATAATGAAATTGCAAATCACTTAGCAGCAAC
TGAAGACAATTATCAACCACGTGGAGAAAATCAAACCGAGCAGGGCTGTGTGAAACATGGTT
GTAATATGCGACTGCGAACACTGAACTCTACGCCACTCCACAAATGATGTTTCAGGTGTCA
TGGACTGTTGCCACCATGTATTGATCCAGAGTTCTTAAAGTTAAAGTTGCACATGATTGTA
TAAGCATGCTTCTTGAGTTAAATTATGTATAAACATAAGTGCATTAGAAATCAAGC
ATAAATCACTCAACTGCAAAAAAAAAAAAAAA

FIGURE 84

MQRLGATLLCLLAAAVPTAPAPAPTATSAPVKPGPALSYPQEATLNEMFREVEELMEDTQ
HKLRSAVEEMEAEEAAKASSEVNLPPSYHNETNTDTKVGNNTIHVHREIHKITNNQTG
QMVFSETVI TSVGDEEGRSHECI IDEDCGPSMYCQFASFQYTCQPCRGQRMLCTRSECCG
DQLCVWGHCTKMATRGSNGTICDNQRDCQPGLCCAFQRGLLFPVCTPLPVEGELCHDPASRL
LDLITWELEPDGALDRCPASCGLLCQPHSHSLVYVCKPTFVGSRDQDGEILLPREVPDEYEYV
GSFMEEVVRQELEDLERSLTEEMALGEPAAAAALLGGEI

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 96-100, 106-110, 121-125, 204-208

Casein kinase II phosphorylation site.

amino acids 46-50, 67-71, 98-102, 135-139, 206-210, 312-316,
327-331

N-myristoylation site.

amino acids 202-208, 217-223

Amidation site.

amino acids 140-144

FIGURE 85

AAGGAGGGCTGGGAGGAAAGAGGTAAGAAAGGTTAGAGAACCTACCTCACATCTCTGGGCTCAGAAGGACTCT
AAGATAACAATAATTTCAGCCCATCCACTCTCCTCCCAAACACACATGTGCATGTACACACACACATACAC
CACACATACACCTCCTCTCCTCACTGAAGACTCACAGTCACTCACTGTGAGCAGGTCAAGAAAAGGACAC
TAAAGCCTAAGGACAGGCTGGCATTACCTCTGAGCTCTTGGCTTGGTGAAGTCAAAAAACATGGGAGGG
CCAGGCACGGTACTCACACCTGTAATCCCAGCATTTGGAGACCGAGGTGAGCAGATCACTTGAGGTCAAGGAG
TTCGAGACCAGCCTGGCAAATGGAGAAACCCCCATCTACTAAAAAATACAAAAATTAGCCAGGAGGGATGGCAG
AGGTGCTGTAACTCCAGCTACTCAGGTGGCTGAGCCAGGAGATCGCTGAATCCAGGAGGGAGGATGCACT
CAGCTGAGTGCACCGCTGCACTCCAGCCTGGGTGACAGAATGAGACTCTGTCTCAAACAAACACAGGGAGGA
GGGGTAGATACTGTTCTGCAACCTCTTAACCTGCATCTCTTCCAGGGCTGCCCTGATGGGCTG
GCAATGACTGAGCAGGCCAGCCCCAGAGGACAAGGAAGAGAAGGCATATTGAGGAGGGCAAGAAGTGA
GTGAGAATGACTGCCCTGGGAGGGTGTCTGGCCCTGGCAGGGTTGCTGACCCCTACCTGCAAACACACA
AAGAGCAGGACTCAGACTCCTTGTAATGGTCCCCTGCCCTGAGCTCCACCATGAGGCTTCTGTTGG
ACTCTTGCTAGCTGGGTGGCTGGTGCACACTGCCACTGTGCCGTGGTACCCCTGGCATGTTCCCTGCC
GTGTGCCTGCCAGATCCGGCCCTGGTATACGCCCGCTCGTCTACCGCGAGGCTACCAACTGTGACTGCAATGA
CCTATTCTGACGGCAGTCCCCCGGCACTCCCCGAGGCCACAGACCCCTGCTCTGCAAGAGCAACAGCATTGT
CCGCTGGGACAGAGTGGACTCTGGCAACTCTCACAGAGCTGGACCTGCTCCAGAACAGCTTTCGGA
TGGCCGAGACTGTGATTCCATGCCCTGCCAGCTGCTGAGCCTGCCACTAGAGGAGAACAGCTGACCCGGCT
GGAGGACACAGCTTGCAGGGCTGCCAGCCTACAGGAACCTATCTCAACCAACACAGCTACCGCATGC
CCCCAGGGCTTTCTGGCCTCAGCAACTTGCTGCGGCTGACCTCAACTCCAACCTCTGAGGGCATTGACAG
CCGCTGGTTGAAATGCTGCCAACCTGGAGATACTCATGATTGGCGGCAACAGGTAGATGCCATCTGGACAT
GAACATCCGGCCCTGGCCAACCTGCGTAGCCTGGCTAGCAGGAGCATGAAACCTGGGGAGATCTCCGACTATGC
CCTGGAGGGCTGCAAAGGCTGGAGAGCCTCTCTTCTATGACAACAGCTGGCCGGTGGCCAGGGACTTTGC
GGAACAGGTGCCGGGCTCAAGTCTCTAGACCTCAACAAGAACCCGCTCCAGGGTAGGGGGGGACTTTGC
CAACATGCTGCACCTTAAGGAGCTGGGACTGAACACATGGAGGAGCTGGCTCCATGACAAGTTGCC
GAACCTCCCGAGCTGACCAAGCTGGACATCACCATAACCCACGGCTGCTTCATCCACCCCCGCC
CCACCTGCCCAAGATGGAGACCCCTCATGCTCAACACACAGCTCTCAGTGCTGCACCAGCAGACGGTGGAGTC
CCTGCCCAACCTGCAAGGAGGTAGGTCTCCACGGCAACCCCATCCGCTGTGACTGTGCTATCCGCTGGGCAATGC
CACGGGACCCGTGTCGCTCATCGAGCCGAATCCACCCGTGTGCGGAGCCTCCAGGCCCTCC
GGTCCGTGAGGTGCCCTTCCGGAGATGACGGACCACTGTTGCCCTCATCTCCCCACGAAGCTCCCC
CCTCCAGGTAGCCAGTGGAGAGAGCATGGTGTGCAATTGCCGGCACTGGCGAACCCGAGATCTACTG
GGTCACCTCCAGCTGGCTTCGACTGACACCTGCCATGCAAGCAGGAGGTACCGGGTGTACCCGAGGGGACCT
GGAGCTGGAGGGTACAGCAGAACAGGGCAGGGTATACACCTGTGTGGCCAGAACCTGGTGGGGTGCACAC
TAAGACGGTTAGTGTGGTTGTGGGCCGTGCTCTCCAGCCAGGCAGGGACGAAGGACAGGGCTGGAGCTCCG
GGTGCAGGAGACCCACCCCATACATCTGCTATCTTGGGTCAACCAACAGTGTCCACCAACCTC
CTGGTCCAGTGCCTCTCCCTCCGGGGCCAGGGGCCACAGCTCTGGCCCTGCCCTGGGAACCCACAGCTA
CAACATTACCCGCTCTTCAGGCCACGGAGTACTGGGCTGCCGTGCAAGTGGCTTGTGATGCCACACCC
GTTGGCTGTGTATGGGCCAGGACAAAGAGGCCACTTCTGCCACAGGACCTAGGGGATGTCCTGGCTCAT
TGCCATCTGGCTCTGGCTCTTCTGCCAGCTGGCAGCTGGCTAGCGGCCACCTTGGCACAGGCCACCCAGGAA
GGGTGGGGTGGGAGGGGCCCTCTCCCTCCAGGCCAGCTGGGCTTCTGGGGCTGGAGTGGCCCTTCTG
GTCTGCTCCCCCTGGCTGCCCTGGAAATCAGGGAGGAAGCTGCCAGATCCTCAGAACAGGGAGACACTGTG
ACCATTGTCTCAAAATTCTTAAGCTCAGCCTGTTCTCAGCAGTAGAGAAATCACTAGGACTACTTT
AGAGAACAGTCTGGGCCAGATGCCCTGCCAGGAAAGGGACATGGACCCACGTGCTTGAGGCCCTGGCAGCTGG
CAAGACAGATGGGCTTGTGGCCCTGGGGGTGCTTCTGAGCCTTGAAGAAAAGTGGCCCTTAACCTCT
CCTCTGCCCCAGAGGCTCTGGCCTGGCTTGGCTGCTCCCTACCTGTGTCCTCCGGCTGCACCCCT
CTCTCTGTACAGTCTCAGTTGCTTCTGTGCTCTGGCAAGGGCTGAAGGAGGCCACTCCATCTC
CTCGGGGGCTGCCCTCAATGTGGAGTGACCCAGCCAGATCTGAAGGACATTGGAGAGGGATGCC
CGCCTCATCTCAGCAGCCTGGCTGGCATTCCGAAGCTGACTTCTATAGGCAATTGTACCTTGTGGAGAA
ATGTGTACACCTCCCCAACCCGATTCACTCTTCTCTGTTGAAAAAATAAAAATAACAATAAA
AAAA

FIGURE 86

MRLLVAPLLLAWVAGATATVPVVPWHVPCPPQCACQIRPWYTPRSSYREATTVDNDLFLTA
VPPALPAGTQTLLLQSNSIVRVDQSELGYLANLTELDLSQNSFSDARCDFHALPQLLSLHL
EENQLTRLEDHSFAGLASLQELYLNHNQLYRIAPRAFSGLSNLLRLHLSNLLRAIDSRWFE
MLPNLEILMIGGNKVDAILDMDNFRPLANLRSILVLAGMNLREISDYALEGLQSLESLSFYDNQ
LARVPRRALEQVPGLKFLDLNKNPLQRVGPGDFANMLHLKELGLNNMEELVSIDKFALVNLP
ELTKLDITNNPRLSFIHPRAFHHLQPQMELMLNNNALSAHQQTVESLPNLQEVLGHGNPIR
CDCVIRWANATGTRVRFIEPQSTLCAEPPDLQRLPVREVPFREMTHCLPLISPRSFPPSLQ
VASGESMVLHCRALAEPEPEIYWVTPAGLRLTPAHAGRRYRVYPEGTLELRRVTAAEAGLYT
CVAQNLVGADETKTVSVVGRALLQPGRDEGGLELRVQETHPYHILLSWVTPPNTVSTNLTW
SSASSLRGQGATALARLPRGTHSYNITRLLQATEYWACLQVAFADAHTQLACVWARTKEATS
CHRALGDRPGLIAILALAVLLAAGLAAHLGTGQPRKGVGGRRLPPAWAFWGWSAPSVRVV
SAPLVLPWNPGRKLPRSSEGETLLPPLSQNS

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 629-648

N-glycosylation site.

amino acids 94-98, 381-385, 555-559, 583-587

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 485-489

Casein kinase II phosphorylation site.

amino acids 46-50, 51-55, 96-100, 104-108, 130-134, 142-146,
243-247, 313-317, 488-492, 700-704

Tyrosine kinase phosphorylation site.

amino acids 532-540

N-myristoylation site.

amino acids 15-21, 493-499, 566-572

Amidation site.

amino acids 470-474, 660-664, 692-696

FIGURE 87

GCAAGCCAAGGGCTGTTGAGAAGGTGAAGAAGTCCGGACCCATGTGGAGGGGGACATTGTGTACCGCCT
CTACATGCGGAGACCATCATCAAGGTGATCAAGTTCATCCTCATCTGCTACACCGTCTACTACGTGCACAA
CATCAAGTTGACGTGGACTGCACCGTGGACATTGAGAGCCTGACGGGCTACCGCACCTACCGCTGCCACCC
CCTGCCACACTCTTCAGATCCTGGCTCCTCTACATCAGCCTAGTCATCTTACGCCATCTGCATGTA
CACACTGTGGTGATGCTACGGCGCTCCCTCAAGAAGTACTCGTTGAGTCGATCCGTGAGGGAGAGCAGCTACAG
CGACATCCCCGACGTCAAGAACGACTTCGCCTCATGCTGCACCTCATTGACCAATACGACCGCTACTCCAA
GCGCTTCGCCGTCTTCGTGGAGGTGAGTGAGAACAGCTGCCAGCTGAACCTCAACAACGAGTGGACGCT
GGACAAGCTCCGGCAGCGCCTCACCAAGAACGCGCAGGACAAGCTGGAGCTGACCTGTTCATGCTCAGTGGCAT
CCCTGACACTGTGTTGACCTGGTGAGCTGGAGGTCCCTCAAGCTGGAGCTGATCCCGACGTGACCATCCCGCC
CAGCATTGCCAGCTCACGGGCCCTCAAGGAGCTGTGGCTCTACCACACAGCGGCCAAGATTGAAGGCCCTGCCT
GGCCTTCTGCCGAGAACCTGCGGGCCTGCACATCAAGTTCACCGACATCAAGGAGATCCGCTGTGGATCTA
TAGCTGAAAGACACTGGAGGGACTGCACCTGACGGGACACCTGAGGCCAGGAACAACCGCTACATCGTATCGA
CGGGCTGCCGGAGCTCAAAGCCTCAAGGTGCTGCCCTCAAGAGAACCTAAGCAAGCTGCCACAGGTGGTAC
AGATGTGGCGTGCACCTGAGACTGAGCTGGAGCTGATCCGCTGCGACCTGGAGCGATCCCATCTCCATTTAGCCT
GAAGATGGCGAACCTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
CCACAACCTGCAAGGAGATTGACCTCAAGGACAACAACCTCAAGACCATCGAGGAGATCATCAGCTCCAGCACCT
GCACCGCCTCACCTGCCCTAACGCTGACCAACCATCGCCTACATCCCCATCCAGATCGGCAACCTCACCAA
CCTGGAGGCCCTCACCTGAGACATCGAGAACGATCCCACCCAGCTCTACTGCCGCAAGCTGCG
CTACCTGGACCTCAGCCACAACAACCTGACCTCCCTCCCTGCCGACATCGGCCCTCTGAGAACCTCCAGAACCT
AGCCATCACGGCAACCGATCGAGACGCTCCCTCCGGAGCTTCCAGTGGCCGAAGCTGCCGGCTGCCACCT
GGGCAACAACGTGCTGAGTCAGTCACTGCCCTCCAGGGTGGCGAGCTGACCAACCTGACGAGATCGAGCTGCCGG
CAACCGCTGGAGTGCTGCCCTGTGGAGCTGGCGAGTGGCCACTGCTCAAGCGCAGCGGCCCTGGTGGAGGA
GGACCTGTTCAACACACTGCCACCCAGGTGAAGGAGCGCTGTGGAGGGCTGACAAGGAGCAGGCCCTGAGCGAG
GCCGCCAGCACAGCAAGCAGCAGGACCGCTGCCAGTCTCAGGCCGGAGGGCAGGCCCTAGCTTCTCCAG
AACTCCGGACAGCCAGGACAGCCTCGGGCTGGCAGGAGCCTGGGCGTTGTGAGTCAGGCCAGAGCGAGA
GGACAGTATCTGTGGGCTGGCCCCCTTCTCCCTGTGAGACTCACGTCCCCCAGGGCAAGTGCTTGAGGAG
AGCAAGTCTCAAGAGCGCAGTATTTGATAATCAGGGCTCCCTCCCTGGAGGCCAGCTCTGCCCAAGGGCTGAG
CTGCCACCAGAGGTCTGGACCCCTACTTTAGTTCTGTGTTAGTTATTTCTCCATCTCCACCTCCCTCATCC
AGATAACTTATACATCCCAAGAAAGTTCAGGCCAGATGGAAGGTGTTCAAGGAAAGGTGGCTGCCCTTTCCCC
TTGCTCTTATTAGCGATGCCGCCGATTTAACACCCACCTGGACTTCAAGCAGAGTGGTCCGGGCGAACCAG
CCATGGGACGGTCACCCAGTGGCCGGCTGGCTCTGCCGCTGCCAGGGAGAGCAGGCCCTCCAGCTGGA
AAGGCCAGGCCCTGGAGCTTGCCTCTCAGTTGTGGCAGTTAGTTTTGTTTTTTTTAATCAA
AAACAATTTTTAAAAAAAGCTTGAAAATGGATGGTTGGGTATTAAAAAAAGAAAAAAACTTAAAAAAA
AAAAGACACTAACGCCAGTGAAGTTGAGTCAGGGCAGGGTGGCAGTTCCCTTGAGCAAAGCAGCCAGACGT
TGAACGTGTTCTTCCCTGGGCCAGGGTGCAGGGTGTCTTCCGGATCTGGTGTGACCTTGGTCCAGGAGTT
CTATTGTTCTGGGAGGGAGGTTTTGTTGTTGTTGTTGTTGTTGTTGTTGCTTGTGTTCTTCTCC
ATGTGCTTGTGGCAGGCACTCATTCTGTGGCTGCGGCCAGAGGGATGTTCTGGAGCTGCCAAGGAGGGAGGAG
ACTCGGGTTGGCTAATCCCCGGATGAACGGTGCCTCATTGCACTCCCTCCCTCGTGCCTGCCCTGCCCTCCA
CGCACAGTGTAAAGGAGCCAAGAGGAGCCACTCGCCCAAGACTTGTGTTCCCCACCTCCCTGCCGATGGGTGT
CCAGTGCCACCGCTGCCCTCCGCTGCTCCATCAGCCCTGCGCCACCTGGTCTTCATGAAGAGCAGACACTTA
GAGGCTGGTGGGAATGGGGAGGTGCCCTGGGAGGGCAGGCAGGGTGGTCCAAGCCGGTTCCCTGGCC
CTGGAGTGACACAGCCAGTGGCACCTGGTGGCTGGAAGCCAACCTGCTTAGATCACTCGGGTCCCCACCT
AGAAGGGTCCCCGCTTAGATCAATCACGTGGACACTAAGGCACGTTTAGAGTCTTGTCTTAATGATTATGT
CCATCCGTCTGTCCGTCCATTGTGTTCTGCGTCGTGTCATTGGATATAATCTCAGAAATAATGCACACTAG
CCTCTGACAAACCATGAAGCAAAATCCGTTACATGTGGGTCTGAACCTGTAGACTCGGTACAGTATCAAATAA
ATCTATAACAGAAAAAA

FIGURE 88

MRQTIIKVIKFILIIICYTVYYVHNIKFDVDCTVDIESLTGYRTYRCAHPLATLFKILASFYI
SLVIFYGLICMYTLWWMLRRSLKKYSFESIREESSYSDIPDVKNDFAFMLHLIDQYDPLYSK
RFAVFLSEVSENKLRLQLNLNNEWTLDKLRQRLTKNAQDKLELHLFMLSGIPDTVFSDLVELEV
LKLELIPDVTIPPSIAQLTGLKELWLYHTAAKIEAPALAFLRENLRALHIKFDTIKEIPLWI
YSLKTLEELHLTGNLSAENNRYIVIDGLRELKRLKVLRLKSNLSPQVVTDVGVHLQKLSI
NNEGTKLIVLNSLKKMANLTELELIRCDLERIPHISIFSLHNLQEIDLKDNNLKTIEEIISFQ
HLHRLTCLKLWYNHIAYIPIQIGNLTNERLYLNRNKIEKIPTQLFYCRKLRYLDLSHNNLT
FLPADIGLLQNLQNLAITANRIETLPPELFQCRKLRALHGNVLQSLPSRVGELTNLTQIE
LRGNRLECLPVELGECPLLKRSGLVVEEDLFNTLPPEVKERLWRADKEQA

Transmembrane domain:

amino acids 51-75 (type II)

N-glycosylation site.

amino acids 262-266, 290-294, 328-332, 396-400, 432-436, 491-495

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 85-89

Casein kinase II phosphorylation site.

amino acids 91-95, 97-101, 177-181, 253-257, 330-334, 364-368,
398-402, 493-497

N-myristoylation site.

amino acids 173-179, 261-267, 395-401, 441-447

FIGURE 89

GCCTGTTGCTGATGCTGCCGTGCGGTACTTGTCATGGAGCTGGCACTGCGGCGCTCTCCCGT
CCCGCGGTGGTGCTGCTGCCGTGCTGGCCTGAACGCAGGAGCTGTCATTGACT
GGCCCACAGAGGAGGGCAAGGAAGTATGGGATTATGTGACGGTCCGCAAGGATGCCTACATG
TTCTGGTGGCTCTATTATGCCACCAACTCCTGCAAGAACTTCTCAGAACTGCCCTGGTCAT
GTGGCTTCAGGGCGGTCCAGGCAGGTTCTAGCACTGGATTTGAAACTTGAGGAAATTGGC
CCCTTGACAGTGATCTCAAACCACGGAAAACCACCTGGCTCCAGGCTGCCAGTCTCCTATT
GTGGATAATCCGTGGCACTGGTTCAGTTATGTGAATGGTAGTGGTGCCTATGCCAAGGA
CCTGGCTATGGTGGCTTCAGACATGATGGTTCTCCTGAAGACCTTCTCAGTTGCCACAAAG
AATTCCAGACAGTTCCATTCTACATTTCTCAGAGTCCTATGGAGGAAAATGGCAGCTGGC
ATTGGTCTAGAGCTTATAAGGCCATTCAAGCGAGGGACCATCAAGTGCAACTTGC
GGGGT TGCCTGGGTGATT CCTGGATCTCCCTGTTGATT CGGTGCTCTCCTGGGGACCTTACCTGT
ACAGCATGTC TCTCGAAGACAAAGGTCTGGCAGAGGTGTCAAGTTGCAGAGCAAGTA
CTGAATGCCGTAAATAAGGGCTCTACAGAGAGGCCACAGAGCTGTGGGGAAAGCAGAAAT
GATCATTGAACAGAACACAGATGGGTGAACCTCTATAACATCTTAACTAAAGCACTCCCA
CGTCTACAATGGAGTCGAGTCTAGAATTCACACAGAGCCACCTAGTTGTCTTCAGCGC
CACGTGAGACACCTACAACGAGATGCCCTAACGCCAGCTCATGAATGCCCATCAGAAAGAA
GCTAAAATTATTCTGAGGATCAATCCTGGGAGGCCAGGCTACCAACGTCTTGAAACA
TGGAGGAGGACTTCATGAAGCCAGTCATTAGCATTGTGGACGAGTTGCTGGAGGCAGGGATC
AACGTGACGGTGTATAATGGACAGCTGGATCTCATCGTAGATACCATGGGTCAAGGAGGC
GGTGCAGGAAACTGAAGTGGCCAGAACTGCCCTAAATTCAAGTCAGCTGAAGTGGAAAGGCC
CTGT ACAGTGACCCCTAAATCTTGAAACATCTGCTTTGTCAAGTCCTACAAGAACCTTGCTT
TACTGGATTCTGAAAGCTGGTCAATGGTTCTGACCAAGGGACATGGCTCTGAAGAT
GATGAGACTGGTGA CTCAGCAAGAATAGGATGGATGGGCTGGAGATGAGCTGGTTGGC
TGGGGCACAGAGCTGAGCTGAGGCCGCTGAAGCTGTAGGAAGGCCATTCTCCCTGTATCT
AACTGGGGCTGTGATCAAGAAGGTTCTGACCAAGCTCTGCAGAGGATAAAATCATTGTCT
GGAGGCAATTGGAAATTATTCTGCTTAAAAACCTAAGATTTTAAAAAATTGAT
TTGTTTGATCAAAATAAGGATGATAATAGATATTAA

FIGURE 90

MELALRRSPVPRWLLLLPLLLGLNAGAVIDWPTEEGKEVWDYVTVRKDAYMFWWLYYATNSC
KNFSELPLVMWLQGGPGGSSTGFGNFEEIGPLSDLKPRKTTWLQAASLLFVDNPVGTGFSY
VNGSGAYAKDLAMVASDMMVLLKTFFSCHKEFQTVPFYIFSESYGGKMAAGIGLELYKAIQR
GTIKCNFAGVALGDSWISPVDVLSWGPYLYSMSLLEDKGLAEVSKVAEQVLNAVNKGLYRE
ATELGKAEMIIEQNTDGVNFYNILTKSTPTSTMESSLEFTQSHLVCLCQRHVRHLQRDALS
QLMNGPIRKKLKIIIPEDQSWGGQATNVFVNMEEDFMKPVISIVDELLEAGINVTVYNGQLDL
IVDTMGQEAWVRKLKWPELPKFSQLWKALYSDPKSLETSAFVKSYKNLAFYWILKAGHMVP
SDQGDMALKMMRLVTQQE

Signal sequence:

amino acids 1-25

N-glycosylation site.

amino acids 64-68, 126-130, 362-366

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 101-105

Casein kinase II phosphorylation site.

amino acids 204-208, 220-224, 280-284, 284-288, 351-355, 449-453

N-myristoylation site.

amino acids 22-28, 76-82, 79-85, 80-86, 119-125, 169-175,
187-193, 195-201, 331-337, 332-338, 360-366

FIGURE 91

GGCCGCGGGAGAGGAGGCCATGGCGCGCGCGGGCGCTGCTGCTGGCGTGCTGGCTC
GGGCTGGACTCAGGAAGCCGGAGTCGCAGGAGGCAGGCCGTTATCAGGACCATGCGGCCGA
CGGGTCATCACGTGCGGCATCGTGGGTGGAGAGGAGCCGAACTCGGGCGTTGGCGTGGCA
GGGGAGCCTGCGCCTGTGGGATTCCCACGTATGCGGAGTGAGCCTGCTCAGCCACCGCTGGG
CACTCACGGCGGCGCACTGCTTGAAACCTATAGTGACCTTAGTGATCCCTCCGGGTGGATG
GTCCAGTTGCCAGCTGACTTCCATGCCATCCTCTGGAGCCTGCAGGCCTACTACACCCG
TTACTCGTATCGAATATCTATCTGAGCCCTCGCTACCTGGGAATTCACCTATGACATTG
CCTTGGTGAAGCTGTCGACCTGTCACTAACACATCCAGCCCCATCTGTCTCCAG
GCCTCCACATTGAGTTGAGAACCGGACAGACTGCTGGGTGACTGGCTGGGGTACATCAA
AGAGGATGAGGCAGTGCATCTCCCCACACCCCTCCAGGAAGTTAGGTGCCATCATAAACAA
ACTCTATGTGCAACCACCTCTCCTCAAGTACAGTTCCGCAAGGACATCTTGGAGACATG
GTTTGTGCTGGCAACGCCAACGGCGGGAGGATGCCTGCTCGGTGACTCAGGTGGACCCCT
GGCCTGTAACAAGAATGGACTGTGGTATCAGATTGGAGTCGTGAGCTGGGAGTGGCTGTG
GTCGGCCAATCGGCCCGGTGTACACCAATATCAGCCACCACTTGAGTGGATCCAGAAC
CTGATGGCCAGAGTGGCATGTCCCAGCCAGACCCCTCCTGCCACTACTCTTTCCCTCT
TCTCTGGCTCTCCACTCCTGGGCCGGTCTGAGCCTACCTGAGCCCATGCAGCCTGGGC
CACTGCCAAGTCAGGCCCTGGTTCTTTCTGTCTTGGTAATAAACACATTCCAGTTGA
TGCCTTGCAGGGCATTCTTCAAAAAAAAAAAAAAAA

FIGURE 92

MGARGALLLALLARAGLRKPESQEAPLSGPCGRRVITSRIVGGEDAEELGRWPWQGSLRLW
DSHVCGVSLLSHRWALTAAHCFETYSDLSDPSGWMVQFGQLTSMPSFWSLQAYYTRYFVSNI
YLSPRYLGNSPYDIALVKLSAPVTYTKHIQPICLQASTFEFENRTDCWVTGWTGYIKEDEALP
SPHTLQEJVQVAIINNSMCNHLFLKYSFRKDIFGDMVCAGNAQGGKDACFGDGGPLACNKNG
LWYQIGVVSWGVGCRPNRPGVYTNIHHFEWIQKLMAQSGMSQPDPSWPLLFFPLLWALPL
LGPV

Signal sequence:

amino acids 1-18

N-glycosylation site.

amino acids 167-171, 200-204, 273-277

Casein kinase II phosphorylation site.

amino acids 86-90, 134-138, 161-165, 190-194, 291-295

N-myristoylation site.

amino acids 2-8, 44-50, 101-107, 225-231, 229-235, 239-245,
259-265, 269-275

Amidation site.

amino acids 33-37

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 252-263,

Serine proteases, trypsin family, histidine active site.

amino acids 78-84

FIGURE 93

CCCCACGCGTCGGCGGACCGTGGGAAGGGCAGAATGGACTCCAAGCCTGCCCTAGGGCT
CTTGCCCTCATCCTCTGGCAAATGCAGTTACAGCCCCGAGCCCACCAGCGGAGGACGC
TGCCCCCAGGCTGGGTGCCCCCTGGCGTGCAGGACCCCTGAGGAAGAGCTGAGTCTCACCTT
GCCCTGAGACAGCAGAAATGTGAAAAGACTCTCGGAGCTGGTGCAGGCTGTGAGGATCCCAG
CTCTCCTCAATACGGAAAATACCTGACCCTAGAGAAATGTGGCTGATCTGGTGAGGCCATCCC
CACTGACCCTCCACACGGTGCAAAAATGGCTCTTGGCAGCCGGAGCCCAGAAGTGCATTCT
GTGATCACACAGGACTTCTGACTTGTGGCTGAGCATCCGACAACAGCAGAGCTGCTGCTCCC
TGGGGCTGAGTTCATCACTATGTGGAGGACCTACGAAACCCATGTTGTAAGGTCCCCAC
ATCCCTACCAGCTCCACAGGCCTGGCCCCCATGTGGACTTTGTGGGGGACTGCACCGT
TTTCCCCAACATCATCCCTGAGGCAACGTCTGAGCCGAGGTGACAGGGACTGTAGGCCT
GCATCTGGGGTAACCCCTCTGTGATCGTAAGCGATAACAACCTGACCTACAAGACGTGG
GCTCTGGCACCAGCAATAACAGCCAAGCCTGTGCCAGTTCCTGGAGCAGTATTTCATGAC
TCAGACCTGGCTCAGTCATGCGCCTCTCGGTGGCAACTTGACATCAGGCATCAGTAGC
CCGTGGTTGGACAACAGGGCCGGGCCGGGATTGAGGCCAGTCTAGATGTGCAGT
ACCTGATGAGTGTGGCTGCCAACATCTCACCTGGTCTACAGTAGCCCTGGCCGGCATGAG
GGACAGGAGCCCTCCTGCAGTGGCTCATGCTCAGTAATGAGTCAGCCCTGCCACATGT
GCATACTGTGAGCTATGGAGATGATGAGGACTCCCTCAGCAGCGCTACATCCAGCGGGTCA
ACACTGAGCTCATGAAGGCTGCCGCTCGGGTCTCACCCCTGCTCTCGCCTCAGGTGACAGT
GGGGCCGGGTGTTGGTCTGTCTCTGGAAAGACACCAGTTCCGCCCTACCTTCCCTGCCCTCAG
CCCCTATGTCACCACAGTGGAGGCACATCCTCCAGGAACCTTCCATCACAAATGAAA
TTGTTGACTATATCAGTGGTGGCTTCAGCAATGTGTTCCCACGGCTTACATACCAAGGAG
GAAGCTGTAACGAAGTTCTGAGCTCTAGCCCCCACCTGCCACCATCCAGTTACTTCATG
CAGTGGCCGTGCCCTACCCAGATGTGGCTGCACTTCTGATGGCTACTGGTGGTCAGCAACA
GAGTGCCCATCCATGGGTGTCGGAACCTCGGCTCTACTCCAGTGTGTTGGGGGATCCTA
TCCTGATCAATGAGCACAGGATCCTAGTGGCCCCCCCTCTGGCTTCTCAACCCAAG
GCTCTACCAGCAGCATGGGGCAGGTCTTTGATGTAACCCGTGGCTGCCATGAGTCTGTC
TGGATGAAGAGGTAGAGGGCCAGGGTTCTGCTCTGGCTGGGATCCTGTAACAGGC
TGGGGAACACCAACTTCCAGCTTGCTGAAGACTCTACTCAACCCCTGACCCCTTCTATC
AGGAGAGATGGCTTGTCCCTGCCCTGAAGCTGGCAGTTCACTCCCTTATTCTGCCCTGTTG
GAAGCCCTGCTGAACCCCTCAACTATTGACTGCTGCAGACAGCTTATCTCCCTAACCTGAAA
TGCTGTGAGCTTGACTTGAACCTCCACCATGCTCCATCATACTCAGGTCTCCCTACT
CCTGCCCTAGATTCCCTCAATAAGATGCTGTAACTAGCATTGGATGCCCTCCCTCCGC
ATCTCATCTTCTCTTCAATCAGGCTTTCCAAAGGGTTGTATACAGACTCTGTGCACTA
TTTCACTTGATATTCACTCCCCAATTCACTGCAAGGAGACCTACTGTCACCGTTACTCT
TTCCTACCCCTGACATCCAGAAACAAATGGCCTCCAGTGCATACTTCTCAATTTGCTTATG
GCCCTTCCATCATAGTTGCCACTCCCTCCCTACTTAGCTTCCAGGTCTTAACCTCTG
ACTACTCTTGTCTTCTCTCATCAATTCTGCTTCTCATGGAATGCTGACCTTCATTG
TCCATTGAGATTTGCTCTCAGTTACTCATTGTCACCGGAAACAAATCACTGACA
TCTACAAACCATTACCATCTCACTAAATAAGACTTCTATCCAATAATGATTGATACTCTAAA
TGTAAAAAA

FIGURE 94

MGLQACLLGLFALILSGKCSYSPEPDQRRTLPPGVSLGRADPEEELSLTFALRQQNVERLS
ELVQAVSDPSSPQYGKYLTLENVADLVRPSPLTLHTVQKWLLAAGAQKCHSVITQDFLTCWL
SIRQAELLPGAEFHYYVGGPTETHVVRSPHYQLPQALAPHVDFVGLHRFPPTSSLRQRP
EPQVTGTVGLHLGVTPSVIRKRYNLTSQDVGSCTSNNSQACAQFLEQYFHDSDLAQFMRLFG
GNFAHQASVARVVGQQGRGRAGIEASLDVQYLMMSAGANISTWVYSSPGRHEGQEFLQWLML
LSNESALPHVHTVSYGDDEDSLSSAYIQRVNTELMKAAARGLTLFASGDSGAGCWSVSGRH
QFRPTFPASSPYVTTVGGTSFQEPFLITNEIVDYISGGGFSNVFPRPSYQEEAVTKFLSSSP
HLPSSYFNASGRAYPDVAALSDGYWVVSNRVPIPWVSGTSASTPVFGGILSLINEHRILSG
RPPLGFLNPRLYQQHGAGLFDVTRGCHESCLDEEVEGQGFCSGPGWDPVTGWGTPTSQLC

Signal sequence:

amino acids 1-16

N-glycosylation site.

amino acids 210-214, 222-226, 286-290, 313-317, 443-447

Glycosaminoglycan attachment site.

amino acids 361-365, 408-412, 538-542

Casein kinase II phosphorylation site.

amino acids 212-216, 324-328, 392-396, 420-424, 525-529

N-myristoylation site.

amino acids 2-8, 107-113, 195-201, 199-205, 217-223, 219-225,
248-254, 270-276, 284-290, 409-415, 410-416, 473-479, 482-488,
521-527, 533-539, 549-555

FIGURE 95

GCCGCGCGCTCTCTCCGGCCCACACCTGTCTGAGCGGCGCAGCGAGCCGGCCCCGGC
GGGCTGCTCGCGCGGAACAGTGCTCGGCATGGCAGGGATTCCAGGGCTCCTCTTCTC
TTCTTCTGCTCTGTGCTGTGGCAAGTGAGCCCTAACAGTCCCCCTGGAAACCCACTG
GCCTGCATAACCGCCTCCCTGTCGTCTGCCCAAGTCTACCCCTCAATTAGCCAAGCCAGACT
TTGGAGCCGAAGCAAATTAGAAGTATCTTCTCATGTGGACCCAGTGTCTAAGGGAACT
CCACTGCCCACTTACGAAGAGGCCAAGCAATATCTGTCTTATGAAACGCTCTATGCCAATGG
CAGCCGCACAGAGACGCAGGTGGCATCTACATCCTCAGCAGTAGTGGAGATGGGCCAAC
ACCGAGACTCAGGGTCTTCAGGAAAGTCTCGAAGGAAGCGGCAGATTATGGCTATGACAGC
AGGTTCAGCATTGGAAAGGACTTCCTGCTCAACTACCCTTCTCAACATCAGTGAAGTT
ATCCACGGGCTGCACCGCACCCCTGGCAGAGAACGATGTCTCACAGCTGCCACTGCA
TACACGATGGAAAACCTATGTGAAAGGAACCCAGAACGCTCGAGTGGCTTCTAAAGCCC
AAGTTAAAGATGGTGGTCGAGGGCCAACGACTCCACTTCAGCCATGCCAGCAGATGAA
ATTCAGTGGATCCGGTGAAACGCACCCATGTGCCAAGGGTGGATCAAGGGCAATGCCA
ATGACATCGGCATGGATTATGATTATGCCCTCTGGAACTCAAAAGCCCCACAAGAGAAA
TTTATGAAGATTGGGGTGAGCCCTCTGCTAAGCAGCTGCCAGGGGAGAATTCACTTCTC
TGGTTATGACAATGACCGACCAGGAATTGGTGTATCGCTCTGTGACGTCAAAGACGAGA
CCTATGACTTGCTCTACAGCAATGCGATGCCAGCCAGGGCCAGCGGTCTGGGTCTAT
GTGAGGATGTGGAAGAGACAGCAGCAGAACGTTATTGGCATTTCAGG
GCACCAAGTGGTGGACATGAATGGTCCCCACAGGATTCAACGTGGCTGTCAAATCACTC
CTCTCAAATATGCCAGATTGCTATTGGATTAAAGGAAACTACCTGGATTGTAGGGAGGGG
TGACACAGTGTCCCTGCAAGCAATTAAAGGTCTTCATGTTCTATTAGGAGAGGCC
AAATTGTTTTGTCTTGCATTGGCGTGCACACGTGTGTGTGTGTGTGTGTAAAGGTGT
CTTATAATCTTACCTATTCTACAATTGCAAGATGACTGGCTTACTATTGAAAAGTG
GTTTGTGTATCATATCATATCATTAAAGCAGTTGAAGGCATACTTTGCATAGAAATAA
AAAAAAACTGATTGGGGCAATGAGGAATATTGACAATTAAAGTTAATCTCACGTTTG
CAAACTTGATTTCATCTGAACATTGTTCAAAGATTATTAATATTAAATATTGGCATA
CAAGAGATATGAAAAAAAAAAAAAA

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FIGURE 96

MAGIPGLLFLLFFLCAVGQVSPYSAPWKPTWPAYRLPVVLQPSTLNLA
KPDFGAEAKLEVS
SSCGPQCHKGTPLPTYEEAKQYLSYETLYANGSRTELQVGIYILSSSGDGAQHRD
SGSSGKS
RRKRQIYGYDSRFSIFGKDFLLNYPFSTSVKLSTGCTGTLVAEKHVLTA
AHCIDHGKTYVK
TQKLRVGFLKP
KFQWIRVKRTHVPKGWI
KG
NANDIGMDYDYA
LLELKPKH
RKFMKIGV
SPPAKQLPG
GRIHFSGYDND
RPGNLVYRFCDV
KDETYDLLYQQCD
AQPGASGSGVY
VRMWKRQQQ
KWERKI
IGIFSGHQ
WVDMNGSPQDF
NVAVRITPL
KYAQICYW
IKGNYLD
CREG

Signal sequence:

amino acids 1-19

N-glycosylation site.

amino acids 93-97, 207-211

Glycosaminoglycan attachment site.

amino acids 109-113, 316-320

Casein kinase II phosphorylation site.

amino acids 77-81, 95-99, 108-112, 280-284, 351-355

N-myristoylation site.

amino acids 159-165, 162-168, 202-208, 205-211, 314-320, 338-344

Serine proteases, trypsin family, histidine active site.

amino acids 171-177

FIGURE 97

GCATGCCCTGGGTCTCTCGAGCCTGCTGCCTGCTCCCCGCCACCAGCCATGGTGGTT
CTGGAGCGCCCCAGCCTGGGTGGGGCTGTCTCGCACCTCACCTCCCTGCTGCTGCTG
GCGTCGACAGCCATCCTCAATGCGGCCAGGATAACCTGTTCCCCAGCCTGTGGGAAGCCCCA
GCAGCTGAACCGGTTGTGGCGCGAGGACAGCACTGACAGCGAGTGGCCCTGGATCGTGA
GCATCCAGAAGAATGGGACCCACCACTGCGCAGGTTCTGCTCACCAAGCCGCTGGGTGATC
ACTGCTGCCACTGTTCAAGGACAACCTGAACAAACCATACCTGTTCTGTGCTGCTGGG
GGCCTGGCAGCTGGGAACCCCTGGCTCTCGGTCCCAGAAGGTGGTGTTGCCTGGGTGGAGC
CCCACCCGTGTATTCTGGAAGGAAGGTGCCTGTGCAGACATTGCCCTGGTGCCTCGAG
CGCTCCATACAGTTCTCAGAGCGGGCCTGCCATCTGCCTACCTGATGCCCTATCCACCT
CCCTCCAAACACCCACTGCTGGATCTCAGGCTGGGGAGCATCCAAGATGGAGTTCCCTTGC
CCCACCCCTCAGACCCCTGCAGAACGCTGAAGGTTCTATCATGACTCGGAAGTCTGCAGCCAT
CTGTACTGGCGGGAGCAGGACAGGGACCCATCACTGAGGACATGCTGTGCCGGCTACTT
GGAGGGGGAGCGGGATGCTTGTCTGGCGACTCCGGGGCCCTCATGTGCCAGGTGGACG
GCGCCTGGCTGCTGGCCGGCATCATCAGCTGGCGAGGGCTGTGCCAGCGAACAGGCC
GGGGTCTACATCAGCCTCTCGCGACCGCTCCTGGGTGGAGAACATGTGCAAGGGTGCA
GCTCCCGGGCGCGCTCAGGGGGTGGGCCCTCAGGGCACCGAGCCAGGGCTCTGGGCC
CCGCGCGCTCCTAGGGCGCAGCGGGACCGGGCTCGGATCTGAAAGGCGGCCAGATCCACA
TCTGGATCTGGATCTGGCGGGCTCGGGCGGTTCCCCCGCCGTAAATAGGCTCATCTACC
TCTACCTCTGGGGGCCCGACGGCTGCTCGGAAAGGAAACCCCTCCCCGACCCGCCGAC
GGCCTCAGGCCCTCCAAGGCATCAGGCCCGCCAACGGCCTCATGTCCCCGCCAAC
GACTTCCGGCCCCGCCCGGGCCCCAGCGCTTTGTGTATATAATGTTAATGATTATT
AGGTATTGTAACCCTGCCACATATCTTATTCTCCAATTCAATAAATTATT
CTCCAAAAAAA

FIGURE 98

></usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA43318
><subunit 1 of 1, 317 aa, 1 stop
><MW: 33732, pI: 7.90, NX(S/T): 1
MVVSGAPPALGGGCLGTFTSLLLLASTAILNAARI
PVPPACGKPQQLNRVVGGEDSTDSEWP
WIVSIQKNGTHHCAGSLLTSRWVITAHC
FKDNLNKPYLFSVLLGAWQLGNPGSRSQKVGV
A
WVEPHPVYSWKEGACADIALVRLERSIQF
SERVLPICLDPASIHLPPNTHCWISGWGSIQDG
VPLPHPQTLQKLKVPIIDSEVC
SHLYWRGAGQGPITEDMLCAGYLEGERDACL
GDSGGPLMC
QVDGA
WLLAGII
SWGEGCAERNRPGVYISLSA
HRSWVEKIVQGVQLRGRAQGGGALRAPSQG
SGAAARS

Signal sequence:

amino acids 1-32

N-glycosylation site.

amino acids 62-66, 96-100, 214-218, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 99

GACGGCTGGCCACCATGCACGGCTCCTGCAGTTCTGATGCTCTGCTGCCGCTACTGCTA
CTGCTGGTGGCCACCACAGGCCCCGTGGAGCCCTCACAGATGAGGAGAAACGTTGATGGT
GGAGCTGCACAACCTCTACCGGGCCCAGGTATCCCCGACGGCCTCAGACATGCTGCACATGA
GATGGGACGAGGAGCTGGCCGCCTCGCCAAGGCCTACGCACGGCAGTGCCTGTGGGCCAC
AACAAAGGAGCGCGGGCGCCGGCGAGAATCTGTTGCCATCACAGACGAGGGCATGGACGT
GCCGCTGGCCATGGAGGAGTGGCACCACGAGCGTGAGCACTACAACCTCAGGCCGCCACCT
GCAGCCCAGGCCAGATGTGGCCACTACACGCAGGTGGTATGGCCAAGACAGAGAGGATC
GGCTGTGGTCCCCACTTCTGTGAGAAGCTCCAGGGTGTGAGGAGACCAACATCGAATTACT
GGTGTGCAACTATGAGCCTCCGGGAACGTGAAGGGAAACGCCCTACCAGGAGGGACTC
CGTGCTCCCAATGTCCCTCTGGCTACCAACTGCAAGAACTCCCTGTGAACCCATCGAAGC
CCGGAAGATGCTCAGGATTGCCTAACCTGGTAACTGAGGCCCATCCTCCGGGACTGA
AGCATCAGACTCTAGGAAAATGGGTACTCCTCTCCCTAGCAACGGGATTCCGGCTTCT
TGGTAACAGAGGTCTCAGGCTCCCTGGCAACCAAGGCTCTGCCTGCTGTGGAAACCCAGGCC
CCAACCTCCTTAGCAACGAAAGACCCGCCCTCCATGGCAACAGAGGCTCACCTGCGTAAC
AACTGAGGTCCCTTCATTTGGCAGCTCACAGCCTGCCCTGGATGAGGAGGCCAGTTA
CCTTCCCCAAATCGACCCATGTTCTATCCAAAATCAGCAGACAAAGTGACAGACAAAACA
AAAGTGCCCTCTAGGAGGCCAGAGAACTCTGGACCCCAAGATGTCCCTGACAGGGCAAG
GGAACCTCCTACCCATGCCAGGAGGCTGAGGCTGAGGCTGAGTTGCCCTCCAGTG
AGGTCTTGGCCTCAGTTTCCAGCCCAGGACAAGCCAGGTGAGCTGCAGGCCACACTGGAC
CACACGGGCACACCTCCTCCAAGTCCCTGCCAATTCCCCAATACCTCTGCCACCGCTAA
TGCCACGGGTGGCGTGCCTGGCTCTGCAGTCGTCCCTGCCAGGTGCAGAGGCCCTGACA
AGCCTAGCGTTGTGTCAGGGCTGAACCTGGCCCTGGTCACTGTGTGGGCCCTCTGGGA
CTACTGCTCCTGCCTCTGGTGTGGCTGGAATCTTCTTGAATGGATACCACTCAAAGGG
TGAAGAGGTCACTGCTCCTCTGTCACTTCCCCACCCCTGCCCCAGCCCTAAACAAGATA
CTTCTGGTTAAGGCCCTCCGGAAGGAAAGGCTACGGGCATGTGCCTCATCACACCCTCC
ATCCTGGAGGCACAAGGCCTGGCTGGCTGCGAGCTCAGGAGGCCCTGAGGACTGCACACC
GGGCCACACCTCTCCTGCCCTCCCTGGTGAAGTCCTGGGGTGGAGGATTGAGGGAGCT
CACTGCCTACCTGGCCTGGGCTGTCTGCCACACAGCATGTGCCTCTCCCTGAGTGCCTG
TGTAGCTGGGATGGGATTCCCTAGGGCAGATGAAGGACAAGCCCCACTGGAGTGGGTTCT
TTTGAGTGGGGAGGCAGGGACGAGGAAGGAAAGTAACCTGACTCTCCAATAAAACCT
GTCCAACCTGTGAA

FIGURE 100

MHGSCSFLMLLPLLLLVATTGPVGALTDEEKRLMVELHNLRYRAQVSPTASDMLHMRWDEELAAFAKAYARQCVWGHNKERGRRGENLFAITDEGMDVPLAMEEWHHEREHYNLSAATCSPGQMCGHYTQVVWAKTERIGCGSHFCEKLQGVEETNIELLVCNYEPPGNVKGKRPYQEGETPCSQCPSGYHCKNSLCEPIGSPEADAQDLPYLVTTEAPSFRATEASDSRKMGTPSSLATGIPAFLVTEVSGSLATKALPAVETQAPTSLATKDPPSMATEAPPCVTTEVPSILAAHSLPSLDEEPVTFPKSTHVPIPKSADKVTDKVPSRSPENSLDPKMSLTGARELLPHAQEEAEAEELPPSSEVLASVFPAQDKPGELQATLDHTGHTSSKSLPNFPNTSATANATGGRALALQSSLPGAEGPDKPSVSVGLNSGPGHVWGPLLGLLLLPLVLAGIF

Signal sequence:

amino acids 1-22

N-glycosylation site.

amino acids 114-118, 403-407, 409-413

Glycosaminoglycan attachment site.

amino acids 439-443

Casein kinase II phosphorylation site.

amino acids 29-33, 50-54, 156-160, 195-199, 202-206, 299-303

N-myristoylation site.

amino acids 123-129, 143-149, 152-158, 169-175, 180-186, 231-237, 250-256

Amidation site.

amino acids 82-86, 172-176

Peroxidases proximal heme-ligand signature.

amino acids 287-298

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 1.

amino acids 127-138

Extracellular proteins SCP/Tpx-1/Ag5/PR-1/Sc7 signature 2.

amino acids 160-172

FIGURE 101

GTAACGTGAGTCAGGCTTTCATGGGAAGCCCCCTCAACAGAACCGGCATTCTCCAAGTTATGGTGGACGT
ACTTCTGTTCTCCCTCTGCTTACATTAGCAGACGGACTTAAGTCACAACAGATTATCTTCT
CAAGGCAAGTCCATGAGCCACCTTCAAAGCCTCGAGAAGTGAACAAACAAATGAATTGGAGACCATTCC
AAATCTGGGACCAAGTCTCGGCAAATATTACACTTCTCTCCTGGCTGGAAACAGGATTGTTGAAATACTCCCTGA
ACATCTGAAAGAGTTCACTGGACCTTAGCAGCAACAATATTCAAGAGCTCCAACACTGCATT
TCCAGCCCTACAGCTCAAATATCTGTATCTCACAGCAACCGAGTCACATCAATGGACCTGGTATTTGACAA
TTTGGCCAACACACACTCCTGTAAAGCTGAACAGGAACCGAATCTCAGCTATCCCACCAAGATGTTAAACT
GCCCAACTGCAACATCTGAATTGAACCGAAACAAGATTTAAAGTAGATGGACTGACATTCCAAGGCCTTGG
TGCTCTGAAAGTCTCTGAAATGCAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAA
CATGGAAATTTGCACTGGACCATAACAACTAACAGAGATTACCAAAGGCTGGCTTACGGCTTGCTGATGCT
GCAGGAACCTCATCTCAGCCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTCTGCCAGAAGCTCAG
TGAGCTGGACCTAACCTCAACTTCAAGGTTAGATGATTCAAGCTCCTGGCTTAAGCTTACTAAATAC
ACTGCACATTGGAAACAAACAGACTCAGCTACATTGCTGATTGTGCCCTCGGGGCTTCCAGTTAAAGACTTT
GGATCTGAAAGAAATGAAATTCCTGGACTTGAAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAG
GCGACTGATACTCCAAGGAAATCGGATCCGTCTTACTAAAAAGCCTCACTGGTTGGATGCATTGGAGCA
TCTAGACCTGAGTGACAACGCAATCATGCTTACAAGGCAATGCATTTCACAAATGAAGAAACTGCAACAAATT
GCATTAAATACATCAACCTTTGTGCAATTGCGATTGCCAGCTAAAGGCTCCACAGTGGTGGCGAAAACAAACCTT
TCAGAGCTTGTAAATGCCAGTTGTGCTGCCCCTCAGCTGCTAAAGGAGAAGCATTGGCTTAGCCAGA
TGGCTTGTGATGATTTCCAAACCCAGATCACGGTTAGCCAGAAACACAGTCGGCAATAAGGTT
CAATTGAGTTCACTGCTCAGCTGCCAGCAGTCAGTCTCCCAATGACTTTGCTTGGAAAAAGACAATGA
ACTACTGCATGATGCTGAAATGAAAATTATGCAACACCTCCGGGCCAAGGTGGCGAGGTGATGGAGTATACAC
CATCCTCGGCTGCGCAGGTGAAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCACTTGGTTC
ATCCTACTCTGCAAAGCCAAGCTTACAGTAAATATGCTTCCCTCATTCAACAGACCCCCATGGATCTCACCAT
CCGAGCTGGGGCATGGCACGCTGGAGTGTGCTGCTGTGGGGCACCCAGCCCCCAGATAGCCTGGCAGAAGGA
TGGGGCACAGACTTCCAGCTGCACGGAGAGACGCATGCATGTGATGCCAGGATGACGTGTTCTTATCGT
GGATGTGAAGATAGAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAAGTATTCAGCAAATGC
AACTCTGACTGCTCTAGAAACACCATCATTGGCCACTGTTGGACCGAATGTAACCAAGGGAGAAACAGC
CGTCTACAGTGCATTGCTGGAGGAAGCCCTCCCTAAACTGAAACTGGACCAAAGATGATGCCATTGGTGGT
AAACCGAGAGGCACTTTTGCACTGGCACGAGCAATCAGCTCTGATTATTGTGGACTCAGATGTCAGTGATGCTGGGAA
ATACACATGTGAGATGCTAACACCCCTGGCAGTGAGAGGAAACCTGCGCCTCAGTGTGATCCCCACTCCAAC
CTGCGACTCCCCCTCAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATGC
CGTGGTTGCTGTGGGGCACGTCAGCTGTGGGTGATCATACACACAAAGGGAGGAATGAAGA
TTGCACTTACCAACACAGATGAGACCAACTGCCAGAGATATTCTAGTTATTGTCATCTCAGGGAACGTT
AGCTGACAGGCAAGATGGTACGTGCTTCAAGAAAGTGGAGGCCACCCAGTTGTGACATCTCAGGTGCTGG
ATTGGTCTTACCAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAGCTGATGGAGCTGC
CACAGATCTGTTCTTGCCGTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGATGGCTCAGA
TCCTTGAACATATCATAAGGTGCTACCCATGTTCTCATCCTCAGAAGAACCTGCGAACGGAGCTCAGTAATATAC
GTGGCTTCACATGTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGACCTGGAATGAAAATCTGTG
TCTAAACAAGTCTCTTAAAGTTAGTTAGTGCACATCCAGGCCAGCGCTGGCTCGAGTAATTCTTCTATGGG
TACCTTGGAAAAGCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTTGGACGCCATCAGATTGTGCTGCC
AAGAGCCTTTATTGAAAGCTCATCTTCCCAAGACTTGGACTCTGGGTGAGAGGAAGATGGGAAAGAAAGGAC
AGATTTCAAGGAAGAAATCACATTGTACCTTAAACAGACTTTAGAAAATACAGGACTCCAATTTCAGTC
TTATGACTTGGACACATGACTGAATGAGACCAAGGAAAAGCTTAACATACACTCAGTGAACCTTATT
AAAGAGAGAGATCTTATGTTAAATGGAGTTATGAAATTAAAGGATAAAATGTTATTATACAGAT
GAACCAAAATTACAAAAGTTATGAAAATTATACACTGGGAATGATGCTCATATAAGAACACCTTTAAACTA
TTTTTAACCTTGTGTTTATGAAAAAAAGTATCTACGTAATTAAATGATATAACATGATTATTTATGTATT
TTATAATGCCAGATTCTTTATGAAAATGAGTTACTAAAGCATTAAATAACCTGCCATTGACCAATT
TTAAATAGAAGTACTTCATTATATTGACATTATTAATAAAATGTGTCATTGAA

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FIGURE 102

MVDVLLFSLCLLFHISRPDLSHNRLSFIKASSMSHLQLSQLREVKLNNNELETIPNLGPVSAN
ITLLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEP
GYFDNLANTLLVLKLNRRNISAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKM
QRNGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYLLMLQELHLSQNAINRISPDAWE
FCQKLSLEDDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLGSSLKTLDLKNNE
ISWTIEDMNGAFSGLDKLRRLILQGNRIRSIITKKAFTGLDALEHLDLSDNAIMSLQGNAFSQ
MKKLQQLHLNTSSLLCDCQLKWLPQWVAENNQSFVNASCAPQLLKGRSIFAVSPDGFVCD
DFPKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNEHHDAEMENYAHLRAQG
GEVMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVAKLTNVMLPSFTKTPMDLTIRAGA
MARLECAAVGHHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFIVDVKIEDIGVYSCQAQN
SAGSISANATLTVLETPSFLRPLLDRTVKGETAVLQCIAGGSPPPQLNWTKDDSPLVVTER
HFFAAGNQLLIIVDSVSDAGKYTCMSNTLGERGNVRLSVIPTPTCDSPQMTAPSLODDG
WATVGVIIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADI PSYLSSQGTLD
RQDGYSSESSESGSHHQFVTSSGAGFFLPQHDSSGTCHIDNSSEADVEAATDLFLCPFLGSTGP
MYLKGNVYGSDFETYHTGCPDPRTVLMHYEPSYIKKKECYPCHPSEESCERSFSNISW
PSHVRKLLNTSYSYSHNEPGMKNLCLNKSSLDFSANPEPASVASSNSFMGTFGKALRRPHLDA
YSSFGQPSDCQPRAFYLKAHSSPDLDGSEEDKERTDFQEENHICTFKQTLENYRTPNFQS
YDLDT

Signal sequence:

amino acids 1-19

Transmembrane domain:

amino acids 746-765

N-glycosylation site.

amino acids 62-66, 96-100, 214-220, 382-386, 409-413, 455-459,
628-632, 669-673, 845-849, 927-931, 939-943, 956-960

Glycosaminoglycan attachment site.

amino acids 826-830

Casein kinase II phosphorylation site.

amino acids 17-21, 39-43, 120-124, 203-207, 254-258, 264-268,
314-318, 323-327, 347-351, 464-468, 548-552, 632-636, 649-653,
671-675, 739-743, 783-787, 803-807, 847-851, 943-947, 958-962,
1013-1017, 1019-1023, 1021-1025

Tyrosine kinase phosphorylation site.

amino acids 607-615

N-myristoylation site.

amino acids 179-185, 197-203, 320-326, 367-373, 453-459, 528-534,
612-618, 623-629, 714-720, 873-879

FIGURE 103

GGGGAGAGGAATTGACCATGTAAAAGGAGACTTTTTGGTGGTGGCTGTTGGTGCCTTGCAAAATG
AAGGATGCAGGACGCAGCTTCCTGGAACCGAACGCAATGGATAAAACTGATTGTGCAAGAGAGAAGGAAGAAC
GAAGCTTTCTTGTGAGCCCTGGATCTAACACAAATGTATATGTGCACACAGGGAGCATTCAAGAATGAAA
TAAACCAGAGTAGACCCCGGGGGTGGTGTGTTCTGACATAAATAATCTTAAAGCAGCTGTTCCCCTCC
CCACCCCCAAAAAAAGGATGATTGAAATGAAGAACCGAGGATTCAAAGAAAAAGTATGTTCATTTTCTC
TATAAAGGAGAAAGTGAAGGAGATATTTGGAAATGAAAAGTTGGGCTTTTGTAAAGTAAAGAAGAAC
GGTGTGGTGGTGTTCCTTCTTTGAATTCCCACAAGAGGAGAGGAATTAAATACATCTGCAAAGAAA
TTTCAGAGAAGAAAAGTTGACCGCGCAGATTGAGGCATTGATTGGGGAGAGAACCGAGCAGACAGTTGGA
TTTGTGCCATGTTGACTAAATTGACGGATAATTGCACTTGGATTCTTCTCATCAACCTCTTTTTAAAT
TTTTATTCTCTTGGTATAAGATCATGCCTTCTCTGTTCTTAACCACCTGGATTCCATCTGGATGTTGCT
GTGATCAGTCTGAAATACAACACTGTTGAATTCCAGAACAGGACCAACACCAGATAATTATGAAATGTTGAACAAGAT
GACCTTACATCCACAGCAGATAATGATAGGTTCTAGGTTAACAGGGCCCTATTGACCCCCCTGCTGTGGTGC
GCTGGCTCTCAACTCTGTGGTGGCTGGCTGGTGGGCTCAGGCTGAGGTTCCGGATGGCATCTCACACACGGCT
GCTGAACCTCCATGAGAACCAAATCCAGATCATCAAAGTGAACAGCTCAAGCAGCTTGAGGCACTTGGAAATCCT
ACAGTTGAGTAGGAACCATATCAGAACCAATTGAAATTGGGCTTCAATGGTCTGGCAACCTAACACTCTGGA
ACTCTTGACAATGCTTACTACCATCCGAATGGAGCTTGTATACTTGTCTAAACTGAAGGAGCTGGTT
GCGAAACAACCCATTGAAAGCATTCCCTTATGTTAACAGAATTCTCTTGCCTGACTAGACTTAGG
GGAATTGAAAAGACTTCATACATCTCAGAAGGTGCCTTGAAGGTCTGTCCAACCTGAGGTTATTGAACCTTGC
CATGTGCAACCTCGGGAAATCCCTAACCTCACACCGCTCATAAAACCTAGATGAGCTGGATCTTCTGGGAATCA
TTTATCTGCCATCAGGCCTGGCTTTCCAGGGTTGATGCACCTCAAAACTGTGGATGATACTGCCCAGAT
TCAAGTGAATGAAACGGAATGCCTTGAACACCTTCAGTCAGTAGTGGAGATCAACCTGGCACACAATAATCTAAC
ATTACTGCCTCATGACCTCTTCACTCCCTTGCATCATCTAGAGCGGATACATTACATCACACCCCTGGAACTG
TAACGTGACATACTGTGGCTCAGCTGGGATAAAAGACATGGCCCTCGAACACAGCTTGTGCCCCGGT
TAACACTCTCCAATCTAAAGGGAGGTACATTGGAGAGCTGACCAGATTACTTCACATGCTATGCTCCGGT
GATTGTGGAGCCCCCTGCAGACCTCAATGTCAGTAGGCATGGCAGCTGAGCTGAAATGTCGGGCTCCACATC
CCTGACATCTGTATCTGGATTACTCCAAATGGAACAGCTGACACATGGGGCGTACAAAGTGCAGTAGCTGT
GCTCAGTGTGATGGTACGTTAAATTCAACAAATGTAACGTGCAAGATACAGGCATGTACACATGTATGGTGGTAA
TTCCGGTTGGGAATACTACTGCTTCAGCCACCCCTGAATGTTACTGCAGCAACCCTACTCTTCTTACTTTTC
AACCGTCACAGTAGAGACTATGAAACCGTCTCAGGAATGGCAGGGACCAAGATAACATGGGGTCCCACCTCC
AGTGGTCAGTGGAGACCAATGTCAGGACCTCTCAGACAGGCAAGGTGACAGAGAAAACCTT
CACCATCCCAGTGAATGATATAAACAGTGGGATCCCAGGAATTGATGAGGTCATGAAGACTACCAAAATCATCAT
TGGGTGTTCTGGCCATCACACTCATGGCTGAGTGTGCTGGTCAATTCTACAAGATGAGGAGACGACCCA
TCGGCAAAACCATCACGCCAACAGGACTGTTGAAATTATAATGTTGAGTGTGAGATTACGGGAGACACACC
CATGGAAAGGCCACCTGCCATGCCTGCTATCGAGCATGAGCACCTAAATCACTACATCACAAATCTCCCTT
CAACCACACAACAGTTAACACAATAATTCAATACACAGTTGAGTCAGTGCATGAACCGTTATTGATCCGAATGAA
CTCTAAAGACAATGTACAAGAGACTCAAATCTAAACATTTACAGAGTTACAAAAACAAACAATCAAAAAAA
GACAGTTATTAAAAATGACACAAATGACTGGCTAAATCTACTGTTCAAAAAGTGTCTTACAAAAAAACAA
AAAAGAAAAGAAATTATTAAATTCTATTGTGATCTAAAGCAGACAAAAA

FIGURE 104

MLNKMTLHPQQIMIGPRFNRALFDPLLVLLALQLLVVAGLVRAQTCPSVCSCSNQFSKVIC
VRKNLREVPDGISTNTRLLNLHENQIQIICKVNSFKHLRHEILQLSRNHIRTIEIGAFNGLA
NLNTLELFDNRLTTIPNGAFVYLSKLKELWLRNNPIESIPSYAFNRIPSLRRLDLGELKRLS
YISEGAFEGLSNLRYLNLCNLREIPNLTPLIKLDELDLSGNHLSAIRPGSFQGLMHLQKL
WMIQSQIQVIERNADFNLQSLVEINLAHNNLTLLPHDLFTPPLHHLERIHLHHNPWCNCDIL
WLSWWIKDMAPSNTACCARCNTPPNLKGRYIGELDQNYFTCYAPVIVEPPADLNTEGMAAE
LKCRASTSLTSVSWITPNGTVMTHGAYKVRIAVLSDGTLNFTNVTVQDTGMYTCMVSNSVGN
TTASATLNVTAATTPFSYFSTVTETMEPSQDEARTTDNNVGPTPVVDWETTNVTTSLTPQ
STRSTEKTFTIPVTDINSGIPGIDEVMKTTKIIIGCFVAITLMAAVMLVIFYKMRKQHHRQN
HHAPTRTVEIINVDDETGDTPMESHLPMPAIEHEHLNHYN SYKSPFNHTTVNTINSIHSS
VHEPLLIRMMNSKDNVQETQI

Signal sequence:

amino acids 1-44

Transmembrane domain:

amino acids 523-543

N-glycosylation site.

amino acids 278-282, 364-368, 390-394, 412-416, 415-419, 434-438,
442-446, 488-492, 606-610

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 183-187

Casein kinase II phosphorylation site.

amino acids 268-272, 417-421, 465-469, 579-583, 620-624

N-myristoylation site.

amino acids 40-46, 73-79, 118-124, 191-197, 228-234, 237-243,
391-397, 422-428, 433-439, 531-537

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FIGURE 105

AGCCGACGCTGCTCAAGCTGCAACTCTGTTGAGTTGGCAGTTCTTCGGTTTCCCTCTGCTGTTGGGGCA
TGAAAGGGCTTCGCCGCCGGAGTAAAAGAAGGAATTGACCGGGCAGCGCAGGGAGGGAGCGCAGCGACCGC
GAGGGCGGGCGTGCACCCCTGGCTGGAAGTTGTGCCGGCCCCGAGCGCAGCGCCGCTGGGAGCTTCGGGTAGA
GACCTAGGCCCTGGACCCGATGAGCGCGCCGAGCCTCCGTGCGCGCCGCGGGTGGGCTGCTGCTG
CGGGTGCCTGGGGCGCTGGCCGGTCCGACAGCGCGGTGCGGGGAACTCGGGCAGCCCTCTGGGTAGCGCC
GAGCGCCCAGTCCCCACTACCTGCCGCTGCCCTGGGGACCTGCTGACTGAGTCAGTCAGGGCTAGCGCGTCTT
CCGAGCCACTCCCGTCTGGTCCGGCTGGACTTAAGTCACACAGATTATCTTCATCAAGGCAAGTTCC
ATGAGCCACCTCAAAGCCTCGAGAAGTGAACACTGAACAACAAATGAATTGGAGACCATCCAATCTGGGACCA
GTCTGGCAAATAATTACACTTCTCTGGCTGGAACAGGATTGTGAAATACTCCCTGAACATCTGAAAGAG
TTTCAGTCCCTGAAACTTGGACCTTAGCAGCAACAATTTCAGAGCTCCAAACTGCAATTCCAGCCCTACAG
CTCAAATATCTGTATCTCAACAGCAACCGAGTCACATCAATGGAACCTGGTATTTGACAATTGGCCAACACA
CTCCTTGTGTTAAAGCTGAACAGGAACCGAACATCTCAGCTATCCCACCAAGATGTTAAACTGCCCAACTGCAA
CATCTCGAATTGAAACGAAACAAGATTAAAATGTAGATGGACTGACATTCCAAGGCCTGGCTCTGAAAGTCT
CTGAAAATGAAAGAAATGGAGTAACGAAACTTATGGATGGAGCTTTGGGGCTGAGCAACATGGAAATTGG
CAGCTGGACCATAACAACCTAACAGAGATTACCAAGGCTGGCTTACGGCTGCTGAGCTGAGGAACCTCAT
CTCAGCAAATGCCATCAACAGGATCAGCCCTGATGCCCTGGAGTTCTGCCAGAAGCTCAGTGAGCTGGACCTA
ACTTCAATCACTTATCAAGGTTAGATGATTCAAGCTTCTGGCTAAGCTACTAAATACACTGCAACATTGGG
AACAAACAGAGTCAGCTACATTGCTGATTGTGCCCTCCGGGGCTTCCAGTTAAAGACTTGGATCTGAAAGAC
AATGAAATTCTGGACTATTGAAGACATGAATGGTCTTCTCTGGGCTTGACAAACTGAGGCGACTGATACTC
CAAGGAAATCGGATCCGTTCTATTACTAAAAAGCCTCACTGGTTGGATGCAATTGGAGCATTGAGCTGAGT
GACAACGCAATCATGTCTTACAAGGCAATGCAATTTCACAAATGAAGAAACTGCAACAAATTGCAATTAAATACA
TCAAGCCTTTGTGCATGCCAGCTAAATGGCTCCACAGTGGTGGCGAAAACAACCTTCAGAGCTTGT
AATGCCAGTTGTGCCATCTCAGCTGCTAAAAGGAAGAACGATTGGCTGTTAGGCCAGATGGCTTGT
GATGATTTCACCAACCCAGATCACGGTCAAGCCAGAAACACAGTCGGCAATAAAAGGTTCCAATTGAGTT
ATCTGCTCAGCTGCCAGCAGCAGTGATTCCCCAATGACTTTGCTGGAAAAAAAGACAATGAACACTGCA
GCTGAAATGAAAATTATGCACACCTCCGGGCCAAGGTGGCAGGGTATACACCACATCTCGGCTG
CGCGAGGTGGAATTGCCAGTGAGGGAAATATCAGTGTGTCATCTCCAATCAGTGGTCTACTCTGTC
AAAGGAAAGCTACAGTAAATATGCTTCCCTCATTCACCAAGACCCCCATGGATCTCACCATCCGAGCTGGGCC
ATGGCACGCTGGAGTGCTGCTGTGGGCCACCCAGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG
TTCCAGCTGACGGGAGGAGACGCACTGCACTGGGAGGATGACGGTGTCTTATCTGGGATGTGAAGATA
GAGGACATTGGGTATACAGCTGCACAGCTCAGAACAGTCAGGAGTATTTCAGCAAATGCAACTCTGACTGTC
CTAGAAACACCATCATTTGCCACTGTTGGACCGAACTGTAACCAAGGGAGAAACAGCCGCTCACAGTGC
ATTGCTGGAGGAAGCCCTCCCCCTAAACTGAACTGGACCAAAAGATGATAGCCCATTGGGGTAACCGAGAGGCAC
TTTTTGACGAGGCAATCAGCTCTGATTATTGAGCTCAGATGTCAGTGATGCTGGAAATACACATGTGAG
ATGCTAACACCCCTGGCACTGAGAGAGGAAACGTGCGCCTCAGTGATCCCCACTCCAACCTGCA
CAGATGACAGCCCCATCGTAGACGATGACGGATGGGCCACTGTGGGTGCTGATCATAGCCGTGTTGCTG
GTGGGGCACGTCACTCGTGTGGGGTCACTATACACACAAGCGGGAGGAATGAAGATTGCA
AACACAGATGAGACCAACTGCCAGAGATTCTAGTTATTGTCATCTCAGGGACGTTAGCTGACAGGCAG
GATGGGTACGTGCTTCAGAAAGCCACCAAGTTGTCACATCTCAGGTGCTGGATTTCCTTACCA
CAACATGACAGTAGTGGACCTGCCATATTGACAATAGCAGTGAAAGCTGATGTTAGCTGCCACAGATCTGTC
CTTGCTCGTTTGGGATCCACAGGCCCTATGTATTGAAAGGGAAATGTGTATGGCTCAGATCTTGTAAACA
TATCATACAGGTGCACTGACCAAGAACAGTTTAATGGACCACTATGAGCCAGTTACATAAGAAAAG
GAGTGCACCCATGTTCTCATCTCAGAAGAACGAGCTCAGTAATATATCGTGGCCTCACAT
GTGAGGAAGCTACTAACACTAGTTACTCTCACAAATGAAGGGACCTGGAATGAAAATCTGTGTC
CTTTAGATTGCAAACTCAGAGGCCAGCGTGGCTGCTCGAGTAATTCTTCATGGGTACCTTGGAAA
GCTCTCAGGAGACCTCACCTAGATGCCATTCAAGCTGGACAGCCATCAGATTGTCAGCCAAGAGCCTT
TTGAAAGCTCATCTTCCCCAGACTGGACTCTGGGAGGAGATGGGAAAGAACAGGACAGATTTCAGGAA
GAAAATCACATTGTACCTTAAACAGACTTTAGAAAACAGACTCAGGACTCCAATTTCAGTCTTATGACTTGGAC
ACATAGCTGAATGAGACCAAGGAAAAGCTTAACATACACTACAGGACTCCAATTTCAGTCTTATGACTTGGAC
CTTATGTTTAAATGGAGTTATGAATTAAAGGATAAAAATGCTTATTATACAGATGAACCAAAATTAC
AAAAAGTTATGAAAATTAACTGGGAATGATGCTCATATAAGAACACCTTTAAACTATTGTTATAATGCCAGA
TTTCTTTTATGGAAAATGAGTTACTAAAGCATTAAATAACCTGCCCTGACCATTTTAAATAGAAGTT
ACTCATTATATTGACATTATTAATAAAATGTGCAATTGAAAAAAAAAAAAAAAAAAAAAA

FIGURE 106

MSAPSLRARAAGLGLLLCAVLGRAGRSDSGGRGELGQPSGVAAERPCPTTCRCLGDLLDCSR
KRLARLPEPLPSWVARLDLSHNRLSFIKASSMSHLQSLREVKLNNNELETIPNLGPVSANIT
LLSLAGNRIVEILPEHLKEFQSLETLDLSSNNISELQTAFPALQLKYLYLNSNRVTSMEPGY
FDNLANTLLVLKLNRRNRISSAIPPKMFKLPQLQHLELNRNKIKNVDGLTFQGLGALKSLKMQR
NGVTKLMGAFWGLSNMEILQLDHNNLTEITKGWLGYGLLMLQELHLSQNAINRISPDWEFC
QKLSLEDDLTFNHLSRLDDSSFLGLSLLNTLHIGNNRVSYIADCAFRLSSLKTLDDLKNNEIS
WTIEDMNGAFSGLDKLRRRLLIQGNRIRSIKKRAFTGLDALEHLDLSDNAIMSLQGNAFSQMK
KLQLQHLNNTSLLCDCQLKWLPOWVAENNQSFVNASCACHPQLKGRSIFA VSPDGVCDDF
PKPQITVQPETQSAIKGSNLSFICSAASSSDSPMTFAWKKDNELLHDAEMENYAHLRAQGGE
VMEYTTILRLREVEFASEGKYQCVISNHFGSSYSVKAKLTVNMLPSFTKTPMDLTIRAGAMA
RLECAAVGHPAPQIAWQKDGGTDFPAARERRMHVMPEDDVFFIVDVKIEDIGVYSCAQNSA
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPVLSLDDGWA
FAAGNQLLIIVDSDVSDAGKYTCEMSNTLGTERGNVRLSVIPTPTCDS PQMTAPS
GSISANATLTVLETPSFLRPLLDRTVTKGETAVLQCIAGGSPPPKNWTKDDSPVLSLDDGWA
TVGVVIIAVVCCVVGTSLVWVVIYHTRRRNEDCSITNTDETNLPADI
Signal sequence:
amino acids 1-27

Transmembrane domain:

amino acids 808-828

N-glycosylation site.

amino acids 122-126, 156-160, 274-278, 442-446, 469-473, 515-519,
688-692, 729-733, 905-909, 987-991, 999-1003, 1016-1020

Glycosaminoglycan attachment site.

amino acids 886-890

Casein kinase II phosphorylation site.

amino acids 99-103, 180-184, 263-267, 314-318, 324-328, 374-378,
383-387, 407-411, 524-528, 608-612, 692-696, 709-713, 731-735,
799-803, 843-847, 863-867, 907-911, 1003-1007, 1018-1022,
1073-1077, 1079-1083, 1081-1085

Tyrosine kinase phosphorylation site.

amino acids 667-675

N-myristoylation site.

amino acids 14-20, 36-42, 239-245, 257-263, 380-386, 427-433,
513-519, 588-594, 672-678, 683-687, 774-780, 933-939

Leucine zipper pattern.

amino acids 58-80, 65-87

FIGURE 107

CAAACCTTGCCTCGCGGAGAGCGCCAGCTGACTTGAATGGAAGGAGCCCGAGCCCGGGAGCGCAGCTGAGAC
TGGGGGAGCGCGTTCGGCCGTGGGCGCCGCTGGCGCGGGCGCAGCAGGAAAGGGAAAGCTGTGGTCTGCC
CTGCTCCACGAGGCGCCACTGGTGTGAACCAGGGAGAGCCCCTGGTGGTCCCGTCCCTATCCCTCTTATATA
GAAACCTTCCACACTGGGAAGGCAGCGCGAGGAGGGCTCATGGTGAAGCAAGGAGGCCGGCTGATCTGAG
GCGCACAGCATTGGAGTTACAGATTTACAGATACCAAATGGAAGGCAGGGAGGCAGAACAGCCTGCCTGGT
TCCATCAGCCCTGGCGCCAGCGCAGCTGACTCGGCACCCCTGCAGGCACCATGGCCAGAGGCCGGTGTGC
TGCTCTGCTGCTGCGCCACAGCTGCACCTGGGACCTGTGCTTGCCTGAGGGCCCCAGGATTGGCCGAA
GTGGCGGCCACAGCCTGAGCCCCGAAGAGAACGAATTGCGGAGGGAGGCCGGTGTACTGAGGCCCTGAGG
AGCCCGGGCTGGCCAGCCGGTCAGCTGCCCGAGACTGTGCCGTGTTCCAGGAGGGCGTGTGGACTGTG
GCGTATTGACCTGCGTGAAGTCCCCGGGGACCTGCTGAGCACACCAACCATCTCTGCAGAACACAACCAGC
TGGAAAAGATCTACCCCTGAGGAGCTCTCCCGCTGCACCCGGTGGAGACACTGAACCTGCAAACAAACCGCTGA
CTTCCCAGGGCTCCAGAGAACAGGCTTGAGCATCTGAGAACCTCAATTACCTGTACTTGGCCAATAACAAGC
TGACCTGGCACCCCGTCTCTGCCAAACGCCCTGATCAGTGTGGACTTTGCTGCCAATCTCACCAAGATCT
ATGGGCTCACCTTGGCAGAACCAAACCTGAGGTCTGTGACCTGCACAAACAAACAAGCTGGCAGACGCCGGC
TGCGGACACATGTCACGGCTCAGCAACGTCAGGTCCTCATCTGTCCAGCAACTTCTGCCACGTGC
CCAAGCACCTGCCCTGCCGTGACAAGCTGCACCTCAAGAACAAACAGCTGGAGAAGATCCCCCGGGGCT
TCAGCGAGCTGAGCAGCTGCGAGCTATACTGCAGAACAAACTACCTGACTGACGAGGGCTGGACAAAGAGA
CCTTCTGGAAGCTCTCAGCCTGGAGTACCTGGATCTGTCCAGCAACAAACCTGTCCTGGTCCAGCTGGCTGC
CGCGCAGCCTGGTGTGCTGCACITGGAGAAGAACGCCATCCGGAGCGTGGACCGAATGTGCTGACCCCCATCC
GCAGCCTGGAGTACCTGCTGCTGCCAGCAACCAGCTGGGGAGCAGGGCATCCACCCACTGGCTTCCAGGGC
TCAAGCGGTTGACACGGTGCACCTGTACAACAACAGCGCTGGAGCGCGTGCCTGGCAGTGGCTGCGCTGC
GCACCCCTCATGATCCTGCACAACCAGATCACAGGCATTGGCGCGAAGACTTGCACCCACTACTTCTGGAGG
AGCTCACCTCAGCTACAACCGCATCACAGCCCACAGGTGCACCGCAGCCTCCGCAAGCTGCCCTGCTGC
GCTCGCTGGACCTGTGGCAACCGCTGCACACGCTGGACCTGGCTGAAATGTCATGTGCTGAAGG
TCAAGCGCAATGAGCTGGTGCCTTGGCACAGAGGGCGCTGGCGGATGGCTCAGCTGCGTGAGCTGTACCTCA
CCAGCAACCGACTGCGCAGCCCTGGGCCCGTGCCTGGTGGACCTGCCCATCTGCAGCTGCTGGACA
TCGCCGGAAATCAGCTCACAGAGATCCCCGAGGGCTCCCGAGTCAGTGTGAGTACCTGTACCTGCAGAACACA
AGATTAGTGGCTGGCCGCAATGCTGCACACGCTGGACCTGGGAGGCTGAAGCAGCTGCAGGTCTTGGACATTGAAGG
TAGAGTTGGTGAATTCCAAAGGAGCGTGGCCCTGGGAAGGAAAAGGAGGAGGAGGAAGAGGAGGAGGAGG
AGGAAGAGGAAACAAAGATAGTGACAAGGTGATGCAGATGTGACCTAGGATGATGGACCGCCGACTTTCTGC
AGCACACGCCCTGTGTGCTGTGAGCCCCCACTCTGCCGTGCTCACACAGAACACCCAGCTGCACACATGAGGCA
TCCCACATGACACGGCTGACACAGTCTCATATCCCCACCCCTCCGACGGCGTGTCCCAGGCCACACATGC
ACACACATCACACCCCTCAAACACCCAGCTCAGCCACACACAACACTACCCCTCAAACCCACAGTCTGTACAC
CCCCACTACCGCTGCCACGCCCTCTGAATCATGCAGGGAGGGCTGCCCTGCCACACAGGCCACCA
TCCCCCTCCCCCTGCTGACATGTGATGCTATGCATACACACCACACACACATGCACAAGTCATGTGCGAA
CAGCCCTCCAAAGCCTATGCCACAGACAGCTTGCCTGCCAGCCAGAACATGCCATAGCAGCTGCCGTGCC
GTCCCATCTGTCGTTCCCTGGAGAAGACACAAGGGTATCCATGCTGTGGCCAGGTGCCACCCCT
GGAACTCACAAAAGCTGGTTTATCCTTCCATCCTATGGGACAGGAGCCTCAGGACTGCTGGCTGCC
TGGCCACCCCTGCTCCTCCAGGTGCTGGGAGTCAGTCAGCTGCTAAGAGTCCCTCCCTGCCACGCCCTGGCAGGACA
CAGGCACTTTCCAATGGGAAGGCCAGTGGAGGAGGATGGGAGAGGCCCTGGGTGCTGCTGGGCCTGGGG
CAGGAGTGAAGCAGAGGTGATGGGGCTGGCTGAGCCAGGGAGGAAGGACCCAGCTGCACCTAGGAGACACCTT
GTTCTCAGGCCTGTGGGGAAAGTCCGGTGCCTTATTTTATCTTAAGGAAAAAAATGATAAAAAT
CTCAAAGCTGATTTCTTGTATAGAAAACATAATAAAAGCATTATCCCTATCCCTGCCAAAAAA

□ 9 9 0 4 5 2 - 0 7 8 0 6

FIGURE 108

MEGEEAEQPAWFHQWPWRPGASDSAPPAGTMAQSRVLLLLLPPQLHLGPVLAVRAPGFGRS
GGHSLSPPEENEFAAEEPVLVLSPEEPGPAAVSCPRDCACSQEGVVDCGGIDLREFPGDLP
EHTNHLSLQNNQLEKIYPEELSRLHRLETLNLQNNRLTSRGLPEKAFEHLTNLNYLYLANNK
LTLAPRFLPNALISVDFAANYLTKIYGLTFGQKPNLRSVYLHNNKLADAGLPDNMFNGSSNV
EVLILSSNFLRHVPKHLPPALYKLHLKNNKLEKIPPGAFSELSSLRELYLQNNYLTDEGLDN
ETFWKLSSLEYLDLSSNNLSRVPAGLPRSLVLLHLEKNAIRSVDANVLPIRSLEYLLLHSN
QLREQGIHPLAFQGLKRLHTVHLYNNALERVPSGLPDRVRLMILHNQITGIGREDFATTYF
LEELNLSYNRITSQPVHRDAFRKLRLRSLDLSGNRLHTLPPGLPRNVHVLKVKRNELAALA
RGALAGMAQLRELYLTSNRLRSRALGPRAWVDLAHLQLLDIAGNQLTEIPEGLPESLEYLYL
QNNKISAVPANAFDSTPNLKIGIFLRFNKLAVGSVVDSAFRRLKHLQVLDIEGNLEFGDISKD
RGRLGKEKEEEEEEEEEEETR

Signal sequence:

amino acids 1-48

N-glycosylation site.

amino acids 243-247, 310-314, 328-332, 439-443

Casein kinase II phosphorylation site.

amino acids 68-72, 84-88, 246-250, 292-296, 317-321, 591-595

N-myristoylation site.

amino acids 19-25, 107-113, 213-219, 217-223, 236-242, 335-341,
477-483, 498-502, 539-545, 548-554

Leucine zipper pattern.

amino acids 116-138, 251-273, 258-280, 322-344, 464-486, 471-493,
535-557

FIGURE 109

GGGAGGGGGCTCCGGGCGCCGCAGCAGACCTGCTCCGCCGCGCCTGCCGCTGTCCCTCCGGAGCGGCAG
CACTAGCCGGCGCGAGGGCTGGGGTCTCGAGACTCTCAGAGGGCGCTCCCATCGCGCCACCACCC
CAACCTGTTCTCGCGCCACTGCCTGCCAGGACCCGCTGCCAACATGGATTTCCTGGCGCTGGT
GCTGGTATCCTCGCTCACCTGCAGGCGGCCAGTTCGACGGAGGTGGCCAGGCAAATAGTGTATCGAT
TGGCCTATGTCGTTATGGTGGAGGATTGACTGCTGCTGGGCTGGCTGCCAGTCTGGGACAGTGTAGGCC
TGTGTGCCAACACGATGCAAACATGGTGAATGTATCGGCCAACAAAGTCAAGTGTATCCTGGTTATGCTGG
AAAAACCTGTAATCAAGATCTAAATGAGTGTGGCTGAAGGCCCGCCCTGTAAGCACAGGTGATGAACACTTA
CGGCAGCTACAAGTCTACTGCTCACCGATAATGCTCATGCCGATGGTCTCTGCTCAAGTGCCCTGACCTG
CTCCATGGCAAACGATGCTAGTGGCTGTGATGTTAAAGGACAAATACGGTGCCAGTGCCTGCCATCCCCTGGCCT
GCACCTGGCTCTGTGGAGGACCTGTGATGTAATGCTACAGGAAGAGCCTCTGCCCTAGATT
TAGGCAATGTCACACTTTGGAGCTACATCTGCAAGTGTCAATGCTCATGCTGAGCTTCGATCTCATGTTATTGGAGG
CAAATATCAATGTCATGACATAGACGAATGCTCACTTGGTCAAGTGCAGCAGCTTGCTGATGTTATAA
CGTACGTGGTCTACAAGTGCACGTTAAAGGAGGATACCGGGTGTGGACTGACTGTTGTGTTATCCTCCAAA
AGTTATGATTGAAACCTCAGGTCCAATTGATGACCAAAGGGAAATGGTACCTTTAAAGGGTACACAGGAAA
TAATAATTGGATTCTGTGATGTTGGAAAGTACTTGGTGGCTCCGAAGACACCATATATTCTCTATCATTACCAA
CAGGCCTACTCTCAAGCCACACAAGACCTACACCAAGCCAACACCAATTCTACTCCACCAACCACCA
CCTGCCAACAGAGCTCAGAACACCTCTACCACCTACACCCAGAACGGCCAACCCAGGACTGACAACATAGC
ACCAGCTGCCAGTACACCTCCAGGAGGGATTACAGTTGACAACAGGGTACAGACAGACCCCTCAGAACACCCAGG
AGATGTGTCAGTGTCTGGTACACAGTTGTAATTGACCATGGACTTGTGGATGGATCAGGGAGAAAGACAA
TGACTTGCACTGGAACCAATCAGGGACCCAGCAGGTGGACAATATCTGACAGTGTGGCAGCCAAGGCC
GGGAAAAGCTGCACGCTTGGTGTACCTCTGGCCCTCATGCAATTGGGACCTGTGCCTGTCATTAGGCA
CAAGGTGACGGGCTGCACCTGGCACACTCCAGGTGTTGTGAGAAAACACGGTGCACGGAGCAGCC
GGGAAGAAATGGTGGCCATGGCTGGAGGAAACACAGATCACCTTGCAGGGGCTGACATCAAGAGGAA
AAGATGATTAAGGGTTGGAAAAAAAGATCTATGATGGAAATTAAAGGAACCTGGATTATTGAGCCTGGAGAAG
AGAAGACTGAGGGCAAACCATTTGATGGTTCAAGTATATGAAGGGTGGCACAGAGAGGGTGGGACAGCTG
TTCTCCATATGCACTAAGAATAGAACAGAGAAACTGGCTTAGACTAGAGTATAAGGGAGCATTCTGGCAGG
GGCATTGTTAGAATACTTCATAAAAAAGAAGTGTGAAAATCTCAGTATCTCTCTCTTCTAAAAAATTAGA
AAAAAATTGTCATTTAAGATGGTTAAAGATGTTCTACCAAGGAAAAGTAACAAATTATAGAATTCCCAA
AGATGTTGTCATCTACTAGTAGTATGCACTGAGGAAATCTTAGAACTAAATAATTGGACAAGGCTTAATTAGG
CATTTCCCTCTGACCTCTAACGGAGAGGGATTGAAAGGGAGAGGCCACCAATGCTGAGCTACTGAAATA
TCTCTCCCTATGGCAATTCTAGCAGTATTAAGAAAAAGGAAACTATTATCCAAAGAGGTATGAGGAC
AGATATTGTTAGTATCTCAGTAATGTCCTAGTGTGGCGGTGTTCAATGTTCTCATGGTAAAGGTATAAGCC
TTTCATTGTCATGGATGATGTTCAAGTTTTTTAAAGAGATCCTCAAGGAACACAGTTAGAGAG
ATTTCATGGGTGCATTCTCTGCTCGTGTGACAAGTTATCTGGCTGCTGAGAAAGAGTGCCTGCC
ACACCGCAGACCTTCCCTCACCTCATCAGTATGATTGCTTCTTATCAATTGGACTCTCCAGGTTCCAC
AGAACAGTAATATTTTGAAACAATAGGTACAATAGAAGGTCTTGTGAGTAACGGCAGAATATGGCTG
AGGGGAAAATAATCATTAAGCCTTGAGTAACGGCAGAATATGGCTGAGATCCATTAAATGGTTCA
TCCTTATGGTCATATAACTGCACAGCTGAAGATGAAAGGGAAAATAATGAAAATTAACTTGT
TGATACATTGCACTAAACTGATGGAAGAAGTTATCCAAAGTACTGTATAACATCTGTTATTATTAATGTTT
CTAAAATAAAATGTTAGTGGTTCCAAATGGCTAATAAAAACAATTATGTAAATAAAACACTGTTAGTAAT

FIGURE 110

MDFLLALVLVSSLYLQAAAEDGRWPRQIVSSIGLCRYGGRIDCCWGWARQSWGQCQPVCQP
RCKHGEICGPNKCKCHPGYAGKTCNQDLNECGLKPRPCKHRCMNTYGSYKCYCLNGYMLMPD
GSCSSALTCSMANCQYGCDVVKGQIRCQCPSPGLHLAPDGRTCDVDECATGRASCPRFRC
VNTEFGSYICKCHKGFDLMLYIGGKYQCHDIDECSLGQYQCSSFARCYNVRGSYKCKCKEGYQG
DGLTCVYIPKVMIEPSGPIHPKGNGTILKGDTGNNNWIPDVGSTWWPPKTPYIPPIITNRP
TSKPTTRPTPKPTPIPTPPPPPPLPTELRTPLPPTPERPTTGLTTIAPAASTPPGGITVDN
RVQTDPQKPRGDVFSLVHSCNFDHGLCGWIKEKDNDLHWEPIRDPAQQYLTVA
KAARLVLPLGRLMHSGDLCLSFRHKVTGLHSCTLQVFVRKHGAHGAALWGRNGGHGWRQTQI
TLRGADIKSESQR

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 273-277

Casein kinase II phosphorylation site.

amino acids 166-170, 345-349

Tyrosine kinase phosphorylation site.

amino acids 199-206

N-myristoylation site.

amino acids 109-115, 125-131, 147-153, 191-197, 221-227, 236-242,
421-427, 433-439, 462-468, 476-482

Aspartic acid and asparagine hydroxylation site.

amino acids 104-116, 186-198, 231-243

Cell attachment sequence.

amino acids 382-385

EGF-like domain cysteine pattern signature.

amino acids 75-87

FIGURE 111

CTTCTTGAAAAGGATTATCACCTGATCAGGTTCTCTGCATTGCCCTTAGATTGTGA
AATGTGGCTCAAGGTCTTCACAACTTCCCTTGCAACAGGTGCTGCTCGGGGCTGA
AGGTGACAGTGCCATCACACACTGTCCATGGCGTCAGAGGTCAAGGCCCTACCTACCCGTC
CACTATGGCTTCCACACTCCAGCATCAGACATCCAGATCATATGGCTATTGAGAGACCCA
ACAATGCCAAATACTTA~~TACTGGGCTCTGTGAATAAGTCTGTGGTCTGACTTGGAAATACC~~
AACACAAGTCACCATGATGCCACCCAA~~TGCATCTGCTTATCAACCCACTGCAGTTCCCT~~
GATGAAGGCAATTACATCGTGAAGGTCAACATT~~CAGGAAATGAACTCTATCTGCCAGTCA~~
GAAGATA~~CACAGT~~ACCGTTGATGATCCTGT~~CACAAAGCCAGTGGTGCAGATT~~CATCCTCCCT
CTGGGGCTGTGGAGTATGTGGGAACATGACCC~~TGACATGCCATGTGGAAAGGGGACTCGG~~
CTAGCTTACCAATGGCTAAAAAATGGGAGACCTGT~~CCACACCAGCTCCACCTACTCCTTT~~
TCCCCAAAACAATACCC~~T~~CATATTGCTCCAGTAACCAAGGAAGACATTGGGAA~~TTACAGCT~~
GCCTGGTGAGGAACCC~~TGTCA~~GAGAATGGAAAGT~~GATATCATTATGCCATCATATATTAT~~
GGACCTTATGGACTTCAAGTGAATTCTGATAAAAGGGCTAAAAGTAGGGGAAGT~~GTTACTGT~~
TGACCTTGGAGAGGCCATCCTATTGATTGTTCTGCTGATTCTCATCCCCCAACACCTACT
CCTGGATTAGGAGGACTGACAATACTACATATCATTAAGCATGGGC~~CTCGCTTAGAAGTT~~
GCATCTGAGAAAGTAGCCCAGAAGACAATGGACTATGTGTGCTGCTTACAACAA~~CATAAC~~
CGGCAGGCAAGATGAAACTCATT~~T~~CACAGTT~~ATCATCA~~TTCCGTAGGACTGGAGAAGCTTG
CACAGAAAAGAAAATCATTGT~~CACCTT~~AGCAAGTATAACT~~GGAA~~ATAT~~CA~~CTATT~~TTTGATT~~
ATATCCATGTGTCTTCTCTT~~CCTATGGAAAAAATATCAACCC~~TACAAAGTT~~TATAAAACAGAA~~
ACTAGAAGGCAGGCCAGAAACAGAATACAGGAAAGCTCAAACATT~~TTCAGGCCATGAAGATG~~
CTCTGGATGACTT~~CGA~~ATATATGAATTGTTGCTTT~~CCAGATGTTCTGGT~~TTCCAGG
ATTCCAAGCAGGTCTGTTCCAGCCTCTGATTG~~TGTATCGGGCAAGATTGCACAGTACAGT~~
GTATGAAGTTATT~~CAGCACATCC~~CTGCCAGCAGCAAGACC~~ATCCAGAGTGA~~ACTTT~~CATGG~~
GCTAAACAGTACATT~~CGAGTGA~~AAATTCTG~~AAGAACATT~~TAAGGAAAACAGTGGAAAAGT
ATATTAA~~TCTGGA~~ATCAGTGAAGAAACCAGGACCAACACCTCTTACTCATTATT~~CCTTTACA~~
TGCAGAATAGAGGCATT~~TATGCAAATTGAACTGCAGGTTTT~~CAGCATATACACAATGT~~CTT~~
GTGCAACAGAAAACATGTTGGGAA~~ATATT~~CCTCAG~~GGAGACTCGTTCTCATGCTGACGG~~
GGAGAACGAAAGTGACAGGGTT~~CCATAAGTTG~~TATGAA~~ATATCT~~ACAAACCTCA
ATTAGTTCTACTCTACACTTCACTATCATCAACACTGAGACTATCCTGCTCACCTACAAA
TGTGGAAACTT~~TACATTGTTG~~CATTTCAGCAGACTT~~GTTTATTAA~~ATT~~TTTATTAGTG~~
TTAAGAATGCTAA~~ATTATGTTCA~~ATT~~TTTATT~~CCAA~~ATTCTATCTTGT~~TATTG~~TACAA~~
CAAAGTAATAAGGATGGTTGT~~CACAAAAACAAA~~ACTATGCCTTCTTTTTCAATCACC
AGTAGTATT~~TTGAGAAGACTTGT~~GAACACTTAAGGAA~~ATGACTATTAAAGT~~CTTATT~~TTTA~~
TTTTTTCAAGGAAAGATGGATTCAAATAAATTATTCTGTTT~~GTTT~~AAAAAAAAAAAAAA

FIGURE 112

MWLKVFTTFLSFATGACSGLKVTVPSHTVHGVRGQALYLPHYGFHTPASDIQIIWLFERPH
TMPKYLLGSVNKSVPDLEYQHKFTMMPPNASLLINPLQFPDEGNYIVKVNIQGNGLTLSASQ
KIQVTVDDPVTKPVVQIHPPSGAVEYVGNMTLTCHEGGTRLAYQWLKNGRPVHTSSTYSFS
PQNNTLHIAPVTKEDIGNYSCLVRNPVSEMESDIIMPIIYYGPYGLQVNNSDKGLKVGEVFTV
DLGEAILFDCSADSHPPNTYSWIRTDNTTYIIKHGPRLEVASEKVAQKTMDYVCCAYNNIT
GRQDETHFTVIITSVGLEKLAQKGKSLSPASITGISLFLIISMCLLFLWKKYQPYKVIKQK
LEGRPETEYRKAQTFSGHEDALDDFGIYEFVAFPDVSGVSRIPSRSPASDCVSGQDLHSTV
YEVIQHIPAQQQDHPE

Signal sequence:

amino acids 1-18

Transmembrane domain:

amino acids 341-359

N-glycosylation site.

amino acids 73-77, 92-96, 117-121, 153-157, 189-193, 204-208,
276-280, 308-312

Casein kinase II phosphorylation site.

amino acids 129-133, 198-202, 214-218, 388-392, 426-430, 433-437

Tyrosine kinase phosphorylation site.

amino acids 272-280

N-myristoylation site.

amino acids 15-21, 19-25, 118-124, 163-167, 203-209, 231-237,
239-245

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 7-18

FIGURE 113

GCAAGCGGCGAAATGGCGCCCTCCGGGAGTCTGCAGTTCCCCTGGCAGTCCTGGTGCTGTT
GCTTGGGGTGCTCCCTGGACGCACGGGCGGCGGAGCAACGTTCGCGTCATCACGGACGAGA
ACTGGAGAGAACTGCTGGAAGGAGACTGGATGATAGAATTTTATGCCCGTGGTCCCTGCT
TGTAAAATCTCAACCGAATGGAAAGTTTGCTGAATGGGAGAAGATCTTGAGGTTAA
TATTGCGAAAGTAGATGTCACAGAGCAGCCAGGACTGAGTGGACGGTTATCATAACTGCTC
TTCCTACTATTATCATTGTAAGATGGTGAATTAGGCGCTATCAGGGTCAAGGACTAAG
AAGGACTTCATAAAACTTATAAGTGTAAAGAGTGGAAAGAGTATTGAGCCCTTCATCATG
GTTTGGTCCAGGTTCTGTTCTGATGAGTAGTATGTCAGCACTTTCAGCTATCTATGTGGA
TCAGGACGTGCCATAACTACTTATTGAAGACCTTGGATTGCCAGTGTGGGATCATATACT
GTTTTGCTTAGCAACTCTGTTTCCGACTGTTATTAGGACTCTGTATGATATTGTGCG
AGATTGCCCTTGTCCCTCAAAAAGGCCAGACACCAGCCATACCCATACCCCTCAAAAAAAT
TATTATCAGAACATCTGCACAACCTTGAAAAAAAGTGGAGGAGGAACAAGAGGCGGATGAAGAA
GATGTTCAGAAGAACAGCTGAAAGTAAAGAAGGAACAACAAAGACTTCCACAGAACATGC
CATAAAGACAACGCTCTGGGTCCATCATTGCCACAGATAATCCTAGTTAAATTTTATAG
TTATCTTAATATTATGATTTGATAAAAACAGAAGATTGATCATTGTTGGTTGAAGTG
AACTGTGACTTTTGAAATTGCAAGGTTCAGTCTAGATTGTCATTAAATTGAAAGAGTCTA
CATTCAGAACATAAAAGCACTAGGTATACAAGTTGAAATATGATTAAGCACAGTATGATG
GTTAAATAGTTCTAATTGTTGAAAAATCGTCCAAGCAATAAGATTATGTATATTGTT
TTAATAATAACCTATTCAAGTCTGAGTTGAAATTACATTCCAAGTATTGCATT
TGAGGTATTTAAGAAGATTTTAGAGAAAATTTCTCATTGATATAATTTTCTG
TTCACTGTGAAAAAAGAAGATATTCCATAATGGAGGTTGGCCATTGTCTCAAG
AAATGTGATTTCAGGACAATTCGGGTCTTTAGAGGTTATTCCAAATTCCCTG
ATTTTAGGTTATGCAACTAAAACTACCTTACATTAATTACAGTTCTACACA
TGGTAATACAGGATATGCTACTGATTAGGAAGTTCATGGTATTCTCTGATTC
CAACAAAGTTGATTCTCTGTATTTTCTGTTTCTTCTACTATGGGTTACATTTTT
CAAATTGGATGATAATTCTTGGAAACATTTTTATGTTTTAGAAACAGTATTTTTTGTT
GTTCAAACGTGAAGTTACTGAGAGATCCATCAAATTGAACAATCTGTTTAATTAAAATT
TTGGCCACTTTTCAGATTTACATCATTCTGCTGAACTTCAACTGAAATTGTTTT
TTCTTTGGATGTGAAGGGTGAACATTCCGTATTTTGTCCTGATGTGAAAAGCCTGGT
TTTTACATTTTGGAAATTCAAAAGAAGCTTAAATATAAAAGTTGCATTCTACTCAGAAAAAG
CATCTTCTTGTATATGTCTTAAATGTATTTTGTCCTCATATACAGAAAGTTCTTAATTGAT
TTTACAGTCTGTAATGCTTGATTAAAATAAAATACATTTTTATATTTTAAAAGACAA
ACTTCATATTATCCTGTGTTCTTCCTGACTGGTAATATTGTGGGGATTCACAGGTAAA
GTCAGTAGGATGGAAACATTTTAGTGTATTTTACTCCTAAAGAGCTAGAATACATAGTT
CACCTTAAAGAAGGGGGAAATCATAAAATACAATGAATCAACTGACCATTACGTAGTAGAC
AATTCTGTAATGTCCCCTTTCTAGGCTCTGTTGGTGAATCCATTAGATTTACAG
TATCGTAATATACAAGTTCTTTAAAGCCCTCTCCTTAGAATTAAATATTGTACCATT
AAAGAGTTGGATGTGTACTGTGATGCCTTAGAAAATATCCTAAAGCACAAAAACCT
TTCTAACCACTTCATTAAAGCTGAAAAAAAAAAAAAAAAAA

FIGURE 114

MAPSGSLAVPLAVLVLLLWGPWTGRRSNVRVITDENWRELLEGDWMIIFYAPWCPACQNL
QPEWESFAEWGEDLEVNIAKVDVTEQPGLSGRFIITALPTIYHCKDGEFRRYQGPRTKKDFI
NFISDKEWKSIEPVSSWFGPGSVLMSMSALFQLSMWIRTCHNYFIEDLGLPVWGSYTVFAL
ATLFSGLLLGLCMIFVADCLCPSKRRRPQPYPYPSKLLSESAQPLKKVEEQEADEEDVSE
EEAESKEGTNKDFPQNAIRQRSLGPSLATDKS

Signal sequence:

amino acids 1-26

Transmembrane domain:

amino acids 182-201

Casein kinase II phosphorylation site.

amino acids 68-72, 119-123, 128-132, 247-251, 257-261

Tyrosine kinase phosphorylation site.

amino acids 107-115

N-myristoylation site.

amino acids 20-26, 192-198

Amidation site.

amino acids 25-29

FIGURE 115

GCGAGTGTCCAGCTCGGGAGACCCGTGATAATTGTTAACTAATTCAACAAACGGGACCCCTT
CTGTGTGCCAGAAACCGCAAGCAGTTGCTAACCCAGTGGACAGGCAGGATGGAAAGAGCGGG
AAGGTCCCTGGCCCAGAGCAGTGTGACACTTCCTCTGTGACCATGAAACTCTGGGTGTCTGC
ATTGCTGATGGCTGGTTGGTGTCTGAGCTGTGAGGCCATTCTCACCTCTATTG
GGCACATGACTGACCTGATTATGCAGAGAAAGAGCTGGTGCAGTCTCTGAAAGAGTACATC
CTTGTGGAGGAAGCCAAGCTTCCAAGATTAAGAGCTGGCCAACAAAATGGAAGCCTTGAC
TAGCAAGTCAGCTGCTGATGCTGAGGGTACCTGGCTACCCGTGAATGCCAACAAACTGG
TGAAGCGGCTAACACACAGACTGGCTGCGCTGGAGGACCTTGTCTGCAGGACTCAGCTGCA
GGTTTATGCCAACCTCTGTGAGCGGCAGTTCTCCCCACTGATGAGGACGGAGATAGG
AGCTGCCAACAGCCCTGATGAGACTTCAGGACACATACAGGCTGGACCCAGGCACAATTCCA
GAGGGGAACCTCCAGGAACCAAGTACAGGCAATGCTGAGTGTGGATGACTGCTTGGATG
GGCGCTCGGCCTACAATGAAGGGACTATTATCATACGGTGTGTGGATGGAGCAGGTGCT
AAAGCAGCTTGATGCCGGGGAGGAGGCCACCAACCAAGTCACAGGTGCTGGACTACCTCA
GCTATGCTGCTTCCAGTTGGGTGATCTGCACCGTGCCTGGAGCTCACCGCCGCTGCTC
TCCCTGACCCAAGCCACGAACGAGCTGGAGGAACTGCGGTACTTGAGCAGTTATTGGA
GGAAGAGAGAGAAAAACGTTAACAAATCAGACAGAACGCTGAGCTAGCAACCCAGAAGGCA
TCTATGAGAGGCCTGTGGACTACCTGCTGAGAGGGATTTACGAGAGCCTCTGCGTGG
GAGGGTGTCAAACGTACAGCAGCTGCTCATTGCCCTTCAAAGAGGAGGACGAGTGGACAGCCGACA
TCGTCAGGTACTACGATGTCATGTCTGATGAGGAAATCGAGAGGATCAAGGAGATCGAAAA
CCTAAACTGCACGAGCCACCGTTGATCCAAGACAGGAGTCCTACTGCGCCAGCTA
CCGGGTTTCCAAAGCTCCTGGCTAGAGGAAGATGATGACCCCTGTTGTGGCCGAGTAAATC
GTGGATGCAGCATATCACAGGGTTAACAGTAAAGACTGCAGAATTGTTACAGGTTGCAAAT
TATGGAGTGGAGGACAGTATGAACCGCACTTCGACTTCTCTAGGCACCTTGTACAGGG
CCTCAAAACAGAGGGAAATAGGTTAGCGACGTTCTTAACATGAGTGTAGAAGCTG
GTGGTGCACCGTCTCCCTGATCTGGGGCTGCAATTGGCTAAGAAGGGTACAGCTGTG
TTCTGGTACAACCTCTGCGGAGCGGGGAAGGTGACTACCGAACAGACATGCTGCCTGCC
TGTGCTTGTGGCTGCAAGTGGTCTCCAATAAGTGGTCCATGAACGAGGACAGGAGTTCT
TGAGACCTTGTGGATCAACAGAACGTTGACTTGACCATCCTTCTGCTCTCCCTGGTC
CTTCAGCCCATGTCAACGTGACAGACACCTTGTATGTTCTTGTATGTTCTATCAGGCT
GATTTTGGAGAAATGAATGTTGTCTGGAGCAGAGGGAGACCATACTAGGGCAGTCCTGT
GTGACTGAAGTCCCAGCCCTTCATTAGCCTGTGCCATCCCTGGCCCCAAGGCTAGGATCA
AAGTGGCTGCAGCAGAGTTAGCTGTCTAGCGCCTAGCAAGGTGCCTTGTACCTCAGGTGTT
TTAGGTGTGAGATGTTCAAGTGAACCAAAGTTCTGATACCTGTTACATGTTGTTTAT
GGCATTCTATCTATTGTGGCTTACAAAAAATGTCCTACAGAAAAAA

FIGURE 116

MKLWVSALLMAWFGVLSCVQAEFFTSIGHMTDLIYAEKELVQSLKEYILVEEAKLSKI KSWA
NKMEALTSKSAADAEGYLAHPVNAYKLVKRLNTDWPALEDLVLQDSAAGFIANLSVQRQFFP
TDEDEIGAAKALMRLQDTYRLDPGTISRGEELPGTKYQAMLSVDDCFGMGRSAYNEGDYYHTV
LWMEQVLKQLDAGEEATTKSQVLDYLSYAVFQLGDLHRALELTRRLSLDPSHERAGGNLR
YFEQLLEEEEREKTLTNQTEAELATPEGIYERPVVDYLPERDVYESLCRGEGVKLTPRRQKRLF
CRYHGNRAPQLLIAPFKEEDEWDSPHIVRYYDVMSEEEIERIKEIAKPKLARATVRDPKTG
VLTVASYRVSKSSWLEEDDPVVARVNRMQHITGLTVKTAELLQVANYGVGGQYEPHDFDS
RRPFDSGLKTEGNRLATFLNYMSDVEAGGATVFPLGAIWPKKGTAVFWYNLLRSGEDYR
TRHAACPVLVGCKWVSNKWFHERGQEFLRPCGSTEV

Signal sequence:

amino acids 1-17

N-glycosylation site.

amino acids 115-119, 264-268

Glycosaminoglycan attachment site.

amino acids 490-494

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 477-481

Casein kinase II phosphorylation site.

amino acids 43-47, 72-76, 125-129, 151-155, 165-169, 266-270,
346-350, 365-369, 385-389, 457-461, 530-534

Tyrosine kinase phosphorylation site.

amino acids 71-80, 489-496

N-myristoylation site.

amino acids 14-20, 131-137, 171-177, 446-452

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 8-19

Leucine zipper pattern.

amino acids 213-235

FIGURE 117

GCAGTATTGAGTTTACTCCTCTTTAGTGGAAAGACAGACCCATAATCCCAGTGTGAGTGAAATTGATTGT
TTCATTTATTACCGTTGGCTGGGGTTAGTTCCGACACCTCACAGTGAAGAGCAGGCAGAAGGGAGTTGTGA
AGACAGGACAATCTTCTTGGGATGCTGGTCTTGGAAAGCCAGCGGCCCTGCTCTGTCTTGGCCTCATGACCC
CAGGTCTCTGGTAAACACTGAAAGCCTACTACTGGCCTGGTGCCATCAATTGATCCTTGAGGCTGTGCC
CCTGGGCACCCACCTGGCAGGGCTACCACCATTCGACTGAGCTCCCTGGCTCTGCTGCCAGCGCTTC
CCCTCATCTTAGGGCTGTCTGGGGTGCAGCCTGAGCCTCTGGGGTTCTGGATCCAGGGGAGGGAGAAC
ATCCCTGTGTGAGGCTGTAGGGGAGCGAGGAGGGCCACAGAACATTGAGAGCTGGTAGACCAAAGTG
ATGAAGACTTCAAACCCCCGATTGTCCCCTACTACAGGGACCCACAAGCCCTACAAGAAGGTGTCAGGACTC
GGTACATCCAGACAGAGCTGGGCTCCGTGAGCGGTTGGCTGGTGTACCTCCCAGCTACACTGTCCA
CTTGGCCGTGGCTGTGAACCGTACGGTGGCCATCACTCCCTCGGTTACTCTACTTCAGTGGCAGCGGGGG
CCCAGGCTCCAGCAGGGATGCAAGGGTGTCTCATGGGATGAGCGGCCCTGGCTCATGTCAAGAGACCTG
GCCACCTTACACACACTTGGGGCCACTACGACTGGTTCTCATCATGCAGGATGACACATATGTGCAGGCC
CCCCCTGGCAGCCCTGGCTGGCCACCTCAGCATCAACCAAGACCTGTACTTAGGCCGGCAGAGGAGTTCATG
GCGCAGCGCAGCAGGGCCGGTACTGTCACTGGGGCTTGGCTACCTGTTGTCACTGGAGTCTCTGCTCGTGC
GGCCACATCTGGATGGCTGGAGGAGACATTCTCAGTGGCCCTGGCTGAGGTGGCTTGAGCCTGCTCATG
ACTCTCTGGCGTGGCTGTCTCACAGCACAGGGCAGCAGTATGCTCATTTGAACTGGCCAAAATAGGG
ACCTGAGAAGGAAGGGAGCTGGCTTCTGAGTGCCTCGCCGTGACCCCTGTCTCCGAAGGTACCCCTCATG
ACCGCTCCACAAACGCTCAGCGCTCTGGAGTTGGAGCGGGTTACAGTAAATAGAACAAACTGCAGGCTCAGA
TCCGGAACCTGACCGTGTGACCCCCGAAGGGGAGGCAGGGCTGAGCTGGCCGTTGGCTCCCTGCTCCTTCA
CACACACACTCTGCTTGTGGACTACTTCAGAGCAGCACACCTCTCCTGTGCAAGATGGGG
CTCCAAGTGCCACTACAGGGGCTAGCAGGGCGAGCTGGTGTGCTGGAGACTGCCCTGGAGCAGCTCA
ATCGGCCTATCAGCCCCGCTGCGCTTCCAGAACCGAGCAGCTGCTCAACGGTATCGGCCTTCGACCCAGCAC
GGGCATGGAGTACACCCCTGGACCTGCTGTGGAATGTGTGACACAGCGTGGCACCGGGGGCCCTGGCTCGCA
GGGTCAGGCTGCTGCGGCCACTGAGCCGGTGGAAATCTACCTATGCCCTATGTCACTGAGGCCACCCAGTGC
AGCTGGTGTGCTGCCACTCTGGTGGCTGAAGCTGCTGCAGCCCCGGTTCTCGAGGCTTGTGAGCCAATGTCC
TGGAGCCACGAGAACATGCTATTGCTACCCCTGGCTGGTCTACGGGCCAGAGAACGGTGGCGTGGAGCTCCAG
ACCCATTCTGGGTGAAGGCTGCAAGCAGCGAGTTAGAGCAGGGTACCCCTGGACGAGGCTGGCTGGCTCG
CTGTGCGAGCAGAGGCCCTTCCAGGTGCGACTCATGGACGTGGTCTGAAGAACGACCCCTGTGGACACTCT
TCTTCTTACACCGTGTGGACAAGGCTGGGCCAGTCTCAACCGCTGCGCATGAATGCCATCTCTGGCT
GGCAGGCCCTTCCAGTCCATITCCAGGAGTTCAATCTGCCCTGTCAACCAAGAGATCACCCCCAGGGCCC
CGGGGGCTGGCCCTGACCCCCCTCCCTGGCTGACCCCTCCGGGGCTCTATAGGGGGAGATTG
ACCGCAGGCTTGTGGAGGGCTGCTTACAACCGTGAACCTGGCGGCCAGGCGGGCTGGCAGGTGAAC
TGGCAGGCCAGGAAGAGGAGGAAGCCCTGGAGGGCTGGAGGTGATGGATGTTTCCCTCCGGTTCTCAGGCTCC
ACCTCTTCGGCCGTAGAGCCAGGGCTGGTGCAGAACGTCTCCCTGCGAGACTGCAGGCCACGGCTCAGTGAAG
AACTTACACCGCTGCCCTCAGAACCTGGAGGGCTAGGGGGCCGTGCCAGCTGGCTATGGCTCTTTG
AGCAGGAGCAGCCAATAGCACTTAGCCCCTGGGGCCCTAACCTCATACCTTGTCTGCCAGCC
CCAGGAAGGGCAAGGCAAGATGGTGGACAGATAGAGAATTGTTGCTGTATTTTAAATATGAAAATGTTATTA
ACATGTCTCTGCC

05450660

FIGURE 118

MRLSSLLALLRPALPLILGLSLGCSLSLLRVSWIQGEGEDPCVEAVGERGGPQNPSRARLD
QSDEDFKPRIVPYYRDPNPKVLRTRYIQTTELGSRERLLVAVLTSRATLSTLAVAVNRTV
AHHFPRLLYFTGQRGARAPAGMQVVSHGDERPAWLMSETLRHLHTFGADYDWFFIMQDDTY
VQAPRLAALAGHLSINQDLYLGRAEEFIGAGEQARYCHGGFGYLLSRSLRLRPHLDGCRG
DILSARPDEWLGRCLIDSLGVGCVSQHQGQQYRSFELAKNRDPEKEGSSAFLSAFAVHPVSE
GTLMYRLHKRFSALELERAYSEIEQLQAQIRNLTVLTPEGEAGLSWPVGLPAPFTPNSRFEV
LGWDYFTEQHTFSCADGAPKCPLQGASRADVGDALETALEQLNRRYQPRLRFQKQRLLNGYR
RFDPARGMEYTLDLLECVTQRGHRRALARRVSLLRPLSVEILPMPYVTEATRVQLVLPLL
VAEAAAAPAFLEAFaanVLEPREHALLTLLVYGPREGGRGAPDPFLGVKAaaaEERRYPG
TRLAWLAVRAEAPSQVRLMDVVKHPVDTLFFLTTVWTRPGPEVLNRCRMNAISGWQAFFP
VHFQEFPALSPQRSPPGPPGAGPDPPSPPGADPSRGAPIGGRFDRQASAEGCFYNADYLAA
RARLAGELAGQEEEALEGLEVMVDVFLRFSGLHLFRAVEPGLVQKFSLRDCSPRLSEELYHR
CRLSNLEGLGGRQLAMALFEQEANST

Signal sequence:

amino acids 1-15

Transmembrane domain:

amino acids 489-507

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-68, 150-154, 322-326, 331-337, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-678

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 119

CGGAGTGGTGCGCCAACGTGAGAGGAAACCGTGCCTGGCTGCCTTCCTGTCCCCAAGCC
GTTCTAGACGCGGGAAAAATGCTTCTGAAAGCAGCTCCTTTGAAGGGTGTATGCTTGG
AAGCATTCTGTGCTTGATCACTATGCTAGGACACATTAGGATTGGTCATGGAAATAGAA
TGCACCACCATGAGCATCATCACCTACAAGCTCTAACAAAGAAGATATCTTGAAAATTCA
GAGGATGAGCCATGGAGCTCAGTAAGAGCTTCGAGTATACTGTATTATCCTGTAAAACC
CAAAGATGTGAGTCTTGGCTGCAGTAAAGGAGACTTGGACCAAACACTGTGACAAAGCAG
AGTTCTTCAGTTCTGAAAATGTTAAAGTGTGAGTCATTAATATGGACACAAATGACATG
TGGTTAATGATGAGAAAAGCTTACAAATACGCCCTTGATAAGTATAGAGACCAATACA
GTTCTCCTGCACGCCCACTACGTTGCTATCATTGAAAACCTAAAGTATTTTGTAA
AAAAGGATCCATCACAGCCTTCTATCTAGGCCACACTATAAAATCTGGAGACCTTGAATAT
GTGGGTATGGAAGGAGGAATTGTCTTAAGTGTAGAATCAATGAAAAGACTTAACAGCCTCT
CAATATCCCAGAAAAGTGTCTGAAACAGGGAGGGATGATTGGAAGATATCTGAAGATAAAC
AGCTAGCAGTTGCCTGAAATATGCTGGAGTATTGCGAGAAAATGCAGAAGATGCTGATGGA
AAAGATGTATTTAATACAAATCTGTTGGCTTCTATTAAAGAGGCAATGACTTACACCC
CAACCAGGTAGTAGAAGGCTGTTGTCAGATATGGCTTTACTTTAATGGACTGACTCCAA
ATCAGATGCATGTGATGTATGGGTATACGCCCTAGGGCATTGGCATATTCAAT
GATGCATTGGTTCTTACCTCAAATGGTTCTGACAATGACTGAGAAGTGGTAGAAAAGCG
TGAATATGATCTTGTATAGGACGTGTGTCATTATTGTAGTAGTAACATACATATCCAA
TACAGCTGTATGTTCTTTCTTAATTGGTGGCACTGGTATAACCACACATTAAAG
TCAGTAGTACATTTAAATGAGGGTGGTTCTTAAACACATGAACATTGAAAT
TGTTGGAAAGAAGTGTGTTAAGAATAATAATTGCAAATAACTATTAAATAATTAT
GTGATAAAATTCTAAATTATGAACATTAGAAATCTGTGGGCACATATTGCTGATTGGTT
AAAAAAATTAAACAGGTCTTAGCGTCTAACAGATATGCAAATGATATCTCTAGTTGTGAATT
TGTGATTAAAGTAAAACCTTAGCTGTGTTCCCTTACTTCTAACACTGATTATGTTCT
AAGCCTCCCCAAGTCCAATGGATTGCCTTCTCAAAATGTACAACTAAGCAACTAAAGAAA
ATTAAAGTGAAGTGAAGGAA

FIGURE 120

MLSESSSFLKGVMLGSIFCALITMLGHIRIGHGNRMHHEHHHLQAPNKEDILKISEDERME
LSKSFRVYCIILVKPKDVSLWAAVKETWTKHCDKAFFSSENVKFESINMDTNMWLMMRK
AYKYAFDKYRDQYNWFFLARPTTFAIIENLKYFLLKKDPSQPFYLGHTIKSGDLEYVGMEGG
IVLSVESMKRLNSLLNIPEKCPEQGGMIWKISEDKQLAVCLKYAGVFAENAEDADGKDVFNT
KSVGLSIKEAMTYHPNQVVEGCCSDMAVTFNGLTPNQMHVMMYGVYRLRAFGHIFNDALVFL
PPNGSDND

Signal sequence:

amino acids 1-33

N-glycosylation site.

amino acids 121-125, 342-346

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 319-323, 464-468

Casein kinase II phosphorylation site.

amino acids 64-132, 150-154, 322-326, 331-335, 368-372, 385-389,
399-403, 409-413, 473-477, 729-733, 748-752

Tyrosine kinase phosphorylation site.

amino acids 736-743

N-myristoylation site.

amino acids 19-25, 23-29, 136-142, 397-403, 441-447, 544-550,
558-564, 651-657, 657-663, 672-672

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 14-25

Cell attachment sequence.

amino acids 247-250

FIGURE 121

CCACCGTCCGATCTTACCAACAAACACTCCTGAGGAGAAAGAAAGAGAGGGAGGGAGAG
AAAAAGAGAGAGAGAGAAACAAAAACCAAAGAGAGAGAAAAATGAATTCATCTAAATCAT
CTGAAACACAATGCACAGAGAGAGGATGCTCTCTCCAAATGTTCTATGGACTGTTGCT
GGGATCCCCATCCTATTCAGTGCTGTTCATCACCAGATGTGTTGACATTCGCAT
CTTCAAACCTGTGATGAGAAAAGTTCAGCTACCTGAGAATTACAGAGCTCTCCTGCT
ACAATTATGGATCAGGTTCAAGAATTGTTGCCATTGAACGGAAATTTCACAGAGCTCAGC
AGCTGCTACTTCTTTCTACTGACACCATTCCCTGGCGTTAAGTTAAAGAAC TGCTCAGC
CATGGGGGCTCACCTGGTGGTTATCAACTCACAGGAGGAGCAGGAATTCCCTTACAAGA
AACCTAAAATGAGAGAGTTTTTATTGGACTGTCAGACCAGGTTGTCAGGGTCAGTGGCAA
TGGGTGGACGGCACACCTTGACAAAGTCTCTGAGCTCTGGATGTAGGGAGGCCAACAA
CATAGCTACCCCTGGAGGACTGTGCCACCATGAGAGACTCTCAAACCCAGGCAAAATTGGA
ATGATGTAACCTGTTCTCAATTATTTGGATTGTGAAATGGTAGGAATAAATCCTTG
AACAAAGGAAAATCTCTTTAAGAACAGAAGGCACAACTCAAATGTGAAAGAACAGGAGCA
AGAACATGCCACACCCACCGCCCCACAGGAGAAATTGTGCGCTGAACTTCAAAGGACTTC
ATAAGTATTGTTACTCTGATACAAATAAAATAAGTAGTTAAATGTTAAAAAAAAAAAAAAA
AAA
AAAAA

10031470660

FIGURE 122

MNSSKSSETQCTERGCFSSQMFLWTVAGIPILFLSACFITRCVVTFRIFQTCDEKKFQLPEN
FTELSCNYGSGSVKNCCPLNWEYFQSSCYFFSTDТИWALSLKNCSAMGAHLVVINSQEEQ
EFLSYKKPKMREFFIGLSDQVVEGQWQWVDGTPLTKSLSFWDVGEPENNIATLEDATMRDSS
NPRQNWNDVTCFLNYFRICEMVGINPLNKGKSL

Signal sequence:

amino acids 1-42

N-glycosylation site.

amino acids 2-6, 62-66, 107-111

Casein kinase II phosphorylation site.

amino acids 51-55, 120-124, 163-167, 175-179, 181-185

N-myristoylation site.

amino acids 15-21, 74-80, 155-161

Prokaryotic membrane lipoprotein lipid attachment site.

amino acids 27-38

FIGURE 123

GGGACTACAAGCCGCGCCGCTGCCCTGGCCCCCTCAGCAACCCTGACATGGCGCTGAGGCGGCACC~~CG~~GAC
TCCGGCTCTCGCCTCGGCTGCCTGACTCTTCCTGCTGCTGTTTCAGGGCTGCCTGATAAGGGCTGTAAATC
TCAAATCCAGCAATCGAACCCCAGTGGTACAGGAATTGAAAGTGTGGAACTGTCTGCATCATTACGGATT~~CG~~
AGACAAGTGACCCAGGATCGAGT~~GA~~AGAAAATTCAAGAT~~GA~~ACAAACCATATGTGTTTTGACAACAAAA
TTCAGGGAGACTGGCGGGCTCGT~~C~~AGAAATACTGGGAAAGACATCCCTGAAGATCTGGAATGTGACACGGAGAG
ACTCAGCCCTTATCGCTGTGAGGTCGTTGCTGAAATGACCGCAAGGAATTGATGAGATTGTGATCGAGTTAA
CTGTGCAAGTGAAGCCAGTGACCCCTGTCTGTAGAGT~~G~~CCGAAGGCTGTACCAGTAGGCAAGAT~~G~~GAACACT~~GC~~
ACTGCCAGGAGAGTGAGGCCACCCCCGGCCTCACTACAGCTGGTATCGCAATGTGATG~~T~~ACCGCCACGGATT
CCAGAGCCAATCCCAGATT~~CG~~CAATTCTTCCACTTAAACTCTGAAACAGGCAC~~TT~~GGTGT~~TC~~ACTGCTG
TTCACAAGGACGACTCTGGCAGTACTACTGCAATT~~CG~~CAATGACGCAGGCTCAGCCAGGTGTGAGGAGCAGG
AGATGGAAGTCTATGACCTGAACATGGCGGAATTATTGGGGGGTCTGGTTGCTGTACTGGCCCTGA
TCACGTTGGC~~A~~TCTGCTGTGCATACAGCTGGCTACTTCATCAACAATAACAGGATGGAGAAAGTTACAAGA
ACCCAGGGAAACAGATGGAGTTAACATCCGCACTGACGAGGAGGGC~~G~~ACTTCAGACACAAGTCATCGTTG
TGATCTGAGACCCGCGGTG~~T~~GGCTGAGAGCGCACAGAGGCCACGTGCACATACCTCTGCTAGAAACTCC~~T~~GTCAA
GGCAGCAGAGCTGATGC~~A~~CTCGGACAGAGCTAGACACTCATT~~CA~~AGGCTT~~T~~GGCCAAAGTTGACCA
CTACTCTTACTCTAACAGCACATGAATAGAAGAAATTTCCTCAAGATGGACCCGGTAAATAACACAA
GGAAGC~~G~~AAACTGGGTGCGTTACTGAGTTGGCTTA~~T~~CTGTTCTGGCCTGAT~~CC~~GGCATGAGTATTAGG
GTGATCTTAAAGAGTTGCTCACGTA~~AA~~ACGCCGTGCTGGGCC~~T~~GTGAAGCAGC~~T~~GGTACCCACTGGTCGTT
CAGCAGCCACGACAGCACCATGTGAGATGGCAGGTGGCTGGACAGCACCAGCAGCGCAT~~CC~~GGGGAAACCC~~A~~
GAAAAGGCTTCTACACAGCAGCCTACTTCATCGGCCACAGACACCACCGCAGTTCTTAAAGGCTCTG
TGATCGGTGTTGCA~~G~~TGTCCATTG~~T~~GGAGAAGCTTTGGATCAGCATT~~T~~GTAA~~AA~~ACACCAAAATCAGGAAG
GTAAATTGGT~~T~~G~~T~~GGAAAGGGATCTGGCTGAGGAACCC~~T~~GCTTGTCCAACAGGGTGT~~C~~AGGATTTAGGAAA
ACCTTCGCTT~~A~~GGCTAAGTCTGAAATGGTACTGAAATATGCTTTCTATGGGTCTTGT~~T~~TATT~~T~~TATAAAATT
TACATCTAAATT~~T~~TGCTAAGGATGT~~T~~TTGATTATTGAAAGAAAATTCTATTAAACTGTA~~A~~ATATATTGT
CATACAA~~T~~GTAAATAACCTATT~~T~~TTAAAAAGTTCAACTTAAGGTAGAAGTTCCAAGCTACTAGT~~G~~TAAAT
TGGAAAATATCAATAATTAGAGT~~T~~TTACCAAGGAATCCTCTCATGGAAAGTTACTGTGATG~~T~~CC~~T~~TTCT
CACACAAGTTT~~T~~AGCCTTTTCACAAGGA~~A~~CTCATACTGT~~T~~ACACATCAGACCATAGTTGCTTAGGAAAC~~CT~~
TAAAAT~~T~~CCAGTTAACGCAATGTTGAAATCAGTTG~~C~~ATCTCTTAAAAGAAAAC~~T~~CTCAGGTTAGCTTGA~~A~~
GCCTCTTCTGAGATGACTAGGACAGTCTG~~T~~ACCCAGAGGCCACCCAGAAGCC~~T~~CA~~G~~ATGTACATACAGATG
CCAGTCAGCTCTGGGT~~T~~GC~~G~~CCAGGCC~~C~~CCGCTAGCT~~C~~ACTGTTGCC~~T~~CGT~~T~~GTGCCAGGAGGCC~~T~~
GCCATCCTGGGCC~~T~~GGCAGTGGCTGT~~T~~CCAGT~~G~~GCTTACTC~~A~~CGTGGCC~~T~~CTGCTT~~C~~ATCCAGCACAGC
TCTCAGGTGGCACTGCAGGGACACTGGTGT~~T~~CCATGTAGCGT~~C~~CAGCTTGGCTCTGTAACAGACCTCT
TTTGGTTATGGCTCACAAAATAGGCCCCAATG~~T~~CTATT~~T~~TTTTAATT~~T~~GGTTAATT~~T~~TTGTT
AAGATTG~~T~~CTAACGGCAAAGGCAATTGGAAATCAAGTCTGCAAGTACAATAACATT~~T~~TTAAAAGAAAATGGAT
CCCAC~~T~~GTT~~C~~CTT~~T~~GGC~~A~~AGAGAAAAGCACCCAGACGCCACAGGGCTCTG~~T~~GC~~A~~TTCAAACAAACCATGAT
GGAGTGGCGGCCAGTCCAGC~~T~~TTAAAGAACGTCAGGTGGAGCAGGCCAGGTGAAAGGCC~~T~~GGCGGGAGGAAAG
TGAAAAGCCTGAATCAAAGCAGTTCTAATT~~T~~GACTTTAATT~~T~~TCATCCGCCGGAGACACTGCT~~CC~~ATT
TGTGGGGGACATTAGCAACATC~~A~~CTCAGAAGCCTGT~~T~~CTCAAGAGCAGGTGTTCTAGCCTCACATGCC~~T~~
GCCGTGCTGGACTCAGGACTGAAGT~~G~~CTG~~T~~AAAGCAAGGAGCTG~~T~~GAGAAGGAGC~~A~~CTCCACTGTG~~T~~GC~~T~~GG
GAATGGCTCTCACTACTCACCTG~~T~~CTTCAGCTTCCAGTGT~~T~~CTGGGTTTTTATACTTTGACAGCTTTTT
AATTG~~C~~ATACATGAGACTGTGTTGACTTTTTAGTTATGTGAAACACTTTGCCGCCAGGCC~~T~~GGCAGAGGCA
GGAAATGCTCCAGCAGTGGCTCAGT~~G~~CTCCCTGGTGT~~T~~GTGCATGGCATCCTGGATG~~T~~CTAGCATGCAAGTT~~C~~
CCTCCATCATTGCCACCTGGTAGAGAGGGATGGCT~~C~~CCACCC~~T~~CAGC~~T~~GGGGATT~~C~~AGCTCCAGGCC~~T~~CC
TCTTGGTTG~~T~~CTAGT~~G~~ATAGGGTACGCTTATTGCCCCCTTCTTATAACCTAAACCTCTACACTAGT~~G~~CCA
TGGGAACCAGGTCTGAAAAGTAGAGAGAAGT~~G~~AAAGTAGAGTCTGGGAAGTAGCTGCCTATAACTGAGACTAGA
CGGAAAAGGAATACTCGTGT~~T~~TTAAGATATGAATGTGACTCAAGACTCGAGGCC~~G~~ATACGAGGCTGTGATTCT
GCCTTGGATGGATGTTGCTGTACACAGATGCTACAGACTTGTACTAACACACCGTAATTGGCATTGTTAAC
CTCATTATAAAAGCTTCAAAAAACCC~~A~~

FOURTY FIVE SIX EIGHT

FIGURE 124

```
></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA77624
><subunit 1 of 1, 310 aa, 1 stop
><MW: 35020, pI: 7.90, NX(S/T): 3
MALRRPPRLRLCARLPDFLLLFRGCLIGAVNLKSSNRTPVVQEFESVELSCIITDSQTSD
PRIEWKKIQDEQTTYVFFDNKIQGDLAGRAEILGKTSLKIWNVTRRDSALYRCEVVARNDRK
EIDEIVIELTVQVKPVTPVCRVPKAVPGKMATLHCQESEGHPRPHYSWYRNDVPLPTDSRA
NPRFRNSSFHLNSETGTLVFTAVHKDDSGQYYCIASNDAGSARCEEQEMEVYDLNIGGIIGG
VLVVVLAVLALITLGICCAYRRGYFINNKQDGESYKNPGKPDGVNYIRTDEEGDFRHKSSFVI
```

Important features of the protein:

Signal peptide:

amino acids 1-30

Transmembrane domain:

amino acids 243-263

N-glycosylation sites.

amino acids 104-107, 192-195

cAMP- and cGMP-dependent protein kinase phosphorylation site.

amino acids 107-110

Casein kinase II phosphorylation site.

amino acids 106-109, 296-299

Tyrosine kinase phosphorylation site.

amino acids 69-77

N-myristoylation sites.

amino acids 26-31, 215-220, 226-231, 243-248, 244-249, 262-267